

95247

STIC-Biotech/ChemLib

From: Chan, Christina
Sent: Wednesday, May 28, 2003 5:23 PM
To: Chen, Shin-Lin; STIC-Biotech/ChemLib
Subject: RE: sequence search: 09/865,018

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

-----Original Message-----

From: **Chen, Shin-Lin**
Sent: Wednesday, May 28, 2003 5:18 PM
To: Chan, Christina
Subject: sequence search: 09/865,018

I need case to work on for next bi-week. Please approve the following **Rush sequence search for 09/865,018**. Thanks!

**SEQ ID Nos. 2, 4 and 6.
amino acid residues 22-88 of SEQ ID Nos. 2, 4 and 6.**

Shin-Lin Chen
AU 1632
CM1 12A15
Mail Box: CM1 12E12
(703) 305-1678

Searcher: Fl. Smith
Phone: _____
Location: _____
Date Picked Up: 5/30/03
Date Completed: 6/3/03
Searcher Prep/Review: 7
Clerical: _____
Online time: 10

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: 6
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____





STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 9143

TO: Shin-Lin Chen
Location: cm1/12e12/12a15
Art Unit: 1632
Tuesday, June 03, 2003

Case Serial Number: 865018

From: Mona Smith
Location: Biotech-Chem Library
CM1-6A01
Phone: 308-3278

mona.smith@uspto.gov

Search Notes

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd

OM protein - protein search, using sw model

Run on: May 30, 2003, 08:58:32 : Search time 8.83e seconds
(without alignments)
991.736 Million cell updates/sec

Title: US-09-865-018b-2_copy_22_88

Perfect score: 383

Sequence: 1 EHPKPSACRNFGVDREEL PLECKYQWEQVEKSLPEFY 67

Scoring table: plognm2

Gapop 10.0, Gapext 0.5

Searched: 383515 seqs, 10223094 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000060000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/us08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCMR.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCMR.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCMR.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCMR.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCMR.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCMR.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUBCMR.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCMR.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	383	100.0	167	8	US-08-902-572-18	Sequence 18, Appl
2	383	100.0	158	8	US-08-902-572-22	Sequence 2, Appl
3	383	100.0	144	8	US-08-902-572-22	Sequence 22, Appl
4	383	100.0	144	8	US-08-902-572-24	Sequence 24, Appl
5	383	100.0	165	8	US-08-902-572-8	Sequence 8, Appl
6	383	100.0	180	8	US-08-902-572-6	Sequence 6, Appl
7	383	100.0	191	8	US-08-902-572-2	Sequence 2, Appl
8	475	97.9	198	10	US-09-865-018-2	Sequence 2, Appl
9	369	96.3	197	10	US-09-865-018-4	Sequence 4, Appl
10	366	95.6	237	8	US-08-902-572-25	Sequence 26, Appl
11	366	95.6	252	8	US-08-902-572-28	Sequence 28, Appl
12	254	44.8	71	8	US-08-902-572-29	Sequence 20, Appl
13	360	94.0	178	10	US-09-865-018-6	Sequence 6, Appl
14	153	39.9	164	9	US-09-221-268-3	Sequence 3, Appl
15	153	39.9	164	9	US-09-221-268-5	Sequence 5, Appl
16	153	39.9	164	10	US-09-865-018-24	Sequence 24, Appl
17	153	39.9	164	10	US-09-865-018-2	Sequence 2, Appl
18	151	39.4	247	10	US-09-945-297-170	Sequence 770, App
19	150	25.1	194	10	US-08-744-507-2	Sequence 2, Appl

Sequence 10, Appl
Sequence 14, Appl
Sequence 12, Appl
Sequence 27, Appl
Sequence 16, Appl
Sequence 13, Appl
Sequence 11, Appl
Sequence 4, Appl
Sequence 26, Appl
Sequence 14, Appl
Sequence 137, App
Sequence 135, App
Sequence 14, Appl
Sequence 7, Appl
Sequence 452, App
Sequence 2, Appl
Sequence 32, App
Sequence 32, App
Sequence 2, Appl
Sequence 4, Appl
Sequence 6, Appl
Sequence 16, Appl
Sequence 261, App
Sequence 9, Appl
Sequence 11, Appl
Sequence 3, Appl
Sequence 8, Appl

20 100 26.1 191 10 US-09-733-507-10
21 82 21.4 137 10 US-09-733-507-14
22 80.5 21.0 212 10 US-09-733-507-12
23 71 18.5 13 10 US-09-865-018-27
24 70.5 18.4 196 10 US-09-733-507-16
25 69 18.0 208 10 US-09-733-507-13
26 68.5 17.9 176 10 US-09-733-507-11
27 66.5 17.4 190 9 US-09-733-507-4
28 66 17.2 13 10 US-09-865-018-26
29 65.5 17.1 398 9 US-10-001-254-14
30 65 17.0 932 9 US-10-072-066-147
31 64 16 444 9 US-10-072-076-135
32 62 16.2 247 9 US-09-868-554-14
33 60 15.7 770 9 US-10-153-668-7
34 60 15.7 770 9 US-10-153-668-452
35 59.5 15.5 256 9 US-09-943-308-2
36 59 15.4 746 9 US-10-153-668-232
37 58.5 15.3 806 12 US-10-003-405-2
38 58 15.3 942 10 US-09-842-287-4
39 58.5 15.3 942 10 US-09-969-528-6
40 58 15.1 201 9 US-09-898-554-16
41 57.5 15.0 58 10 US-09-205-658-261
42 57.5 15.0 480 4 US-09-844-414A-9
43 57.5 15.0 814 10 US-09-843-435A-11
44 57 14.9 1493 10 US-09-858-754-3
45 57 14.9 1493 12 US-10-000-864-8

ALIGNMENTS

RESULT 1

US-08-902-572-18
Sequence 18, Application US/08902572
Patent No. US2002068706A1
GENERAL INFORMATION:
APPLICANT: Gyuris, Jeno
APPLICANT: Lamphere, Lou
APPLICANT: Beach, David H.
TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
TITLE OF INVENTION: RELATED THERETO
NUMBER OF SEQUENCES: 34
CORRESPONDENT'S ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109 2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-WINDOWS/MS-DOOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION: US/09/502,572
FILING DATE: 29 Jun 1997
CLASSIFICATION: 514
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/POCKET NUMBER: MIV-069,03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 532-1000
TELEFAX: 617 532-7000
E-MAIL: N. For Seq. 10 N. 14
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-902-572-18

MOLECULE TYPE: Protein
US-08-902-572-24

Query Match 100.0% Score 383; DB 8; Length 348;
Best Local Similarity 100.0%; Pred. No. 2, 4e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACPNLFGPVVHHELTDLKHCDFMEFASQKWNFDQNHKPLEGKYEWQVEVK 60
DB 22 EHPKPSACPNLFGPVVHHELTDLKHCDFMEFASQKWNFDQNHKPLEGKYEWQVEVK 81
QY 61 GSLPEFY 67
DB 82 GSLPEFY 88

RESULT 5

US-08-902-572-8
Sequence 2, Application US/08902572

Patent No. US20020068706A1
GENERAL INFORMATION:

APPLICANT: Gyuris, Jenö
APPLICANT: Lamphere, Lou
TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
TITLE OF INVENTION: RELATED THERETO
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-08-902-572
FILING DATE: 29-JUL-1997

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: MIV-069-03
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 365 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-902-572-2

Query Match 100.0% Score 383; DB 8; Length 365;
Best Local Similarity 100.0%; Pred. No. 2, 6e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACPNLFGPVVHHELTDLKHCDFMEFASQKWNFDQNHKPLEGKYEWQVEVK 60
DB 189 EHPKPSACPNLFGPVVHHELTDLKHCDFMEFASQKWNFDQNHKPLEGKYEWQVEVK 248

QY 61 GSLPEFY 67

DB 249 GSLPEFY 255

RESULT 6

US-08-902-572-6

Sequence 2, Application US/08902572

Patent No. US20020068706A1
GENERAL INFORMATION:

APPLICANT: Gyuris, Jenö
APPLICANT: Lamphere, Lou

APPLICANT: Beach, David H.
TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND

TITLE OF INVENTION: RELATED THERETO
NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELLIOT LLP

STREET: One Post Office Square
CITY: Boston
STATE: MA

COUNTRY: USA
ZIP: 02109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/902,572
FILING DATE: 29-JUL-1997

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: MIV-069-03
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 380 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

US 08 902 572-6

Query Match 100.0% Score 383; DB 8; Length 380;

Best Local Similarity 100.0%; Pred. No. 2, 7e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACPNLFGPVVHHELTDLKHCDFMEFASQKWNFDQNHKPLEGKYEWQVEVK 60
DB 294 EHPKPSACPNLFGPVVHHELTDLKHCDFMEFASQKWNFDQNHKPLEGKYEWQVEVK 263

QY 61 GSLPEFY 67

DB 264 GSLPEFY 270

RESULT 7

US-08-902-572-2

Sequence 2, Application US/08902572
Patent No. US20020068706A1

GENERAL INFORMATION:
APPLICANT: Gyuris, Jenö

APPLICANT: Lamphere, Lou
APPLICANT: Beach, David H.

TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
TITLE OF INVENTION: RELATED THERETO

NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
STREET: One Post Office Square
CITY: Boston

STATE: MA
COUNTRY: USA

ZIP: 02109-2170
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

Db 22 DRPKSACRNLFGPVDHEELTRLEKHCRCMEASQRKNWDFQNHKPLKCKYEWQVEVK 81

QY 61 GSLPEFY 67
|||||
Db 82 GSLPEFY 88

RESULT 10

US-08-902-572-26
Sequence 26, Application US/08902572
Patent No. US20020068706A1
GENERAL INFORMATION:
APPLICANT: Gyuris, Jeno
APPLICANT: Lamphere, Lou
APPLICANT: Beach, David H.
TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
TITLE OF INVENTION: RELATED THERETO
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08-902-572
FILING DATE: 29-JUL-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-069 03
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-902-572-26

Query Match 95.6%, Score 366, DB 8, Length 237;
Best Local Similarity 95.5%, Prod. No. 1.6e-35,
Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0,

QY 1 EHPKPSACRNLFGPVDHEELTRLEKHCRCMEASQRKNWDFQNHKPLKCKYEWQVEVK 60
Db 9 DYAKPSACRNLFGPVDHEELTRLEKHCRCMEASQRKNWDFQNHKPLKCKYEWQVEVK 68
QY 61 GSLPEFY 67
|||||
Db 69 GSLPEFY 75

RESULT 11

US-08-902-572-28
Sequence 28, Application US/08902572
Patent No. US20020068706A1
GENERAL INFORMATION:
APPLICANT: Gyuris, Jeno
APPLICANT: Lamphere, Lou
APPLICANT: Beach, David H.
TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
TITLE OF INVENTION: RELATED THERETO

NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,572
FILING DATE: 29-JUL-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-069.03
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-902-572-28

Query Match 95.6%, Score 366, DB 8, Length 252;
Best Local Similarity 95.4%, Prod. No. 1.7e-35;
Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EHPKPSACRNLFGPVDHEELTRLEKHCRCMEASQRKNWDFQNHKPLKCKYEWQVEVK 60
Db 9 DYAKPSACRNLFGPVDHEELTRLEKHCRCMEASQRKNWDFQNHKPLKCKYEWQVEVK 68
QY 61 GSLPEFY 67
|||||
Db 69 GSLPEFY 75

RESULT 12

US-08-902-572-20
Sequence 20, Application US/08902572
Patent No. US20020068706A1
GENERAL INFORMATION:
APPLICANT: Gyuris, Jeno
APPLICANT: Lamphere, Lou
APPLICANT: Beach, David H.
TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
TITLE OF INVENTION: RELATED THERETO
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,572
FILING DATE: 29-JUL-1997
CLASSIFICATION: 514

Query Match 39.9%; Score 153; DB 9; Length 164;
 Best Local Similarity 44.3%; Pred. No. 1.5e-10;
 Matches 27; Conservative 10; Mismatches 24; Indels 0; Gaps 0;
 QY 7 ACNLEGPVDHEELTRDLEKHCPRMFEPAQPKWNRDFONHKPLEGKYEWQVEVEKGSLEPF 66
 ||| ||| ||| ||| ||| : : : ||| ||| ||| : : : |||
 Db 17 ACNLEGPVDSEQLSRDUALMAGTQFAPERNWEDVTETPLEGFAWEVPVGLGLPKL 76
 QY 67 Y 67
 Db 77 Y 77

Search completed: May 30, 2003, 09:05:09
 Job time : 6.8385 secs

Genforce version 5.1.6
Copyright (c) 1993-2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003 09:52:12 : Search time 42.4884 seconds
(without alignments)
604 482 Million cell updates/sec

Title: US-09-865-018b-2

Perfect score: 1064

Sequence: 1 MSNVRVNSGSLERMARQ PNAISVVEIFKKHLEPPEQT 104

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 90470 seqs 13456425 residues

Total number of hits satisfying chosen parameters: 90470

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database: A_Genoseq_101009.*

1:	/SID52/gqdata/geneseq/geneseq-emb1/AA1960.DAT.*
2:	/SID52/gqdata/geneseq/geneseq-emb1/AA1961.DAT.*
3:	/SID52/gqdata/geneseq/geneseq-emb1/AA1962.DAT.*
4:	/SID52/gqdata/geneseq/geneseq-emb1/AA1963.DAT.*
5:	/SID52/gqdata/geneseq/geneseq-emb1/AA1964.DAT.*
6:	/SID52/gqdata/geneseq/geneseq-emb1/AA1965.DAT.*
7:	/SID52/gqdata/geneseq/geneseq-emb1/AA1966.DAT.*
8:	/SID52/gqdata/geneseq/geneseq-emb1/AA1967.DAT.*
9:	/SID52/gqdata/geneseq/geneseq-emb1/AA1968.DAT.*
10:	/SID52/gqdata/geneseq/geneseq-emb1/AA1969.DAT.*
11:	/SID52/gqdata/geneseq/geneseq-emb1/AA1970.DAT.*
12:	/SID52/gqdata/geneseq/geneseq-emb1/AA1971.DAT.*
13:	/SID52/gqdata/geneseq/geneseq-emb1/AA1972.DAT.*
14:	/SID52/gqdata/geneseq/geneseq-emb1/AA1973.DAT.*
15:	/SID52/gqdata/geneseq/geneseq-emb1/AA1974.DAT.*
16:	/SID52/gqdata/geneseq/geneseq-emb1/AA1975.DAT.*
17:	/SID52/gqdata/geneseq/geneseq-emb1/AA1976.DAT.*
18:	/SID52/gqdata/geneseq/geneseq-emb1/AA1977.DAT.*
19:	/SID52/gqdata/geneseq/geneseq-emb1/AA1978.DAT.*
20:	/SID52/gqdata/geneseq/geneseq-emb1/AA1979.DAT.*
21:	/SID52/gqdata/geneseq/geneseq-emb1/AA1980.DAT.*
22:	/SID52/gqdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SID52/gqdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1064	100.0	198	17	AA092709 Human p27 Kipl.
2	1064	100.0	198	19	AAW29717 27 kDa protein inh
3	1064	100.0	198	19	AAW46888 Amino acid sequence
4	1064	100.0	198	20	AA090768 CK1/KIP protein p2
5	1064	100.0	198	21	AA097523 Human p27 protein
6	1064	100.0	198	21	AA096052 Human cyclin depen
7	1064	100.0	198	21	AA096066 Human cyclin depen
8	1064	100.0	198	21	AA094400 Human p27(Kipl) ki
9	1064	100.0	198	22	AA094545 Amino acid sequence
10	1064	100.0	198	22	AA094809 Human p27 protein.

11	1064	100.0	198	23	AA047880 p27-Kipl
12	1061	99.7	198	21	AA070307 Human mutant cyclin
13	1059	99.5	391	18	AAW46844 Cdk inhibitory fus
14	1059	99.5	391	20	AAW46844 Human p27-p16 fus
15	1059	99.5	391	21	AA097526 Human W3 protein s
16	1059	99.5	391	21	AA096041 Antiproliferative
17	1059	99.5	391	21	AA096068 Angiogenesis inh
18	1057	99.3	198	17	AA079133 Human kipl p27-ki
19	1054	99.1	365	18	AAW23536 CDK inhibitory fus
20	1054	99.1	365	20	AAW95107 Human p16p27 fus
21	1054	99.1	365	20	AAW95096 Human p16p27 fus
22	1054	99.1	365	21	AA097523 Human W3 protein s
23	1054	99.1	365	21	AA096044 Antiproliferative
24	1054	99.1	365	21	AA096071 Angiogenesis inh
25	1054	99.1	365	18	AAW23535 Cdk inhibitory fus
26	1054	99.1	365	20	AAW95095 Human p16(GSp27 f
27	1054	99.1	365	21	AA097528 Human W3 protein s
28	1054	99.1	365	21	AA096043 Antiproliferative
29	1054	99.1	365	21	AA096070 Angiogenesis inh
30	1047	98.4	365	21	AA097527 Human W4 protein s
31	1047	98.4	365	21	AA096042 Antiproliferative
32	1047	98.4	365	21	AA096069 Angiogenesis inh
33	1044	98.1	194	20	AAW94930 Amino acid sequenc
34	976	91.7	198	23	AAW51589 Porcine p27Kipl po
35	931	87.5	197	16	AAW79132 Murine kipl p27-k
36	931	87.5	197	17	AAW92708 Mouse p27 Kipl. M
37	931	87.5	197	19	AAW92718 27 kDa protein inh
38	931	87.5	197	20	AAW08819 Mouse wild type p2
39	931	87.5	197	20	AAW08847 Murine wild type p
40	931	87.5	197	22	AAW4650 Amino acid sequenc
41	908	85.3	334	21	AAW46547 Human W8 protein s
42	908	85.3	334	21	AAW46547 Antiproliferative
43	908	85.3	334	21	AAW46547 Angiogenesis inh
44	908	85.3	334	21	AAW46547 Angiogenesis inh
45	905.5	85.2	348	20	AAW95104 Truncated p27/p16

ALIGNMENTS

RESULT 1
AA094780
17 AA094780 standard, Protein, 198 AA.
XX
AA092709;
XX
16-Jul-1996 (first entry)
XX
Human p27 Kipl.
XX
p27 protein: Kipl, cyclin E, Cdk2; cell proliferation; ulcer;
XX
cancer, hyperplasia, diagnosis, therapy.
XX
Homo sapiens.
XX
W09602140-A1.
XX
01-FEB-1996.
XX
07-JUN-1995: 95W0-US07361.
XX
15-JUL-1994: 94US-0275983.
XX
(HUTCHINSON) HUTCHINSON CANCER RES CENT FRED.
XX
(SLOAN) SLOAN KETTERING INST CANCER RES.
XX
Kell A. Massague J. Polyak K. Roberts JM,
XX
W09602140-A1.
XX
N-PSDB: AAT15336.
XX
p27, an inhibitor of cyclin E Cdk2 complex activation, and agents
XX
which enhance and inhibit its activity, useful for treating

XX PS Disclosure; Columns 17-18, 14pp, English.

XX CC The present sequence represents a p27KIP1 protein, which is part of a

CC family of small cyclin-dependent kinase inhibitors. The proliferative

CC state of a cell transformed with human papillomavirus (HPV) can be

CC evaluated in the following manner: Cyclin/cyclin-dependent kinase

CC complexes containing protein p27KIP1 are isolated from the transformed

CC cell, and the HPV E7 oncoprotein (AAW46886) added to the isolated

CC protein. Cyclin/cyclin-dependent kinase complexes are isolated from an

CC untransformed cell that is substantially homogenic with the transformed

CC cell, and the HPV E7 oncoprotein added. The kinase activities of the 2

CC samples are measured, where a proliferating transformed cell has a

CC greater kinase activity than the untransformed cell. The method is

CC used for determining the extent of interaction and/or inactivation

CC between a cyclin/cyclin-dependent kinase inhibitor and the HPV E7

CC oncoprotein and thus evaluating the proliferative state of a transformed

CC cell.

XX SQ Sequence 198 AA:

Query Match 100.0%; Score 1064; DB 19; Length 198;

Best Local Similarity 100.0%; Pred. No. 7.2e-100;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSNVVSGSPSLERMDARQAEHPKPSACRNLFPGVDHEELTRDLEKHCRDMEASQKWK 60

DB 1 MSNVVSGSPSLERMDARQAEHPKPSACRNLFPGVDHEELTRDLEKHCRDMEASQKWK 60

QY 61 NFDQNHKPLEGKYEWQVEKGSIPFFYYPPPPPKGACKVPAQESQDVSGSPFAAPLIG 120

DB 61 NFDQNHKPLEGKYEWQVEKGSIPFFYYPPPPPKGACKVPAQESQDVSGSPFAAPLIG 120

QY 121 AFANSEDLHLVDPKTDPSDSQTGLAEQACAGIRKRPATDDSSSTONKRANRTEENVSDGSPN 180

DB 121 AFANSEDLHLVDPKTDPSDSQTGLAEQACAGIRKRPATDDSSSTONKRANRTEENVSDGSPN 180

QY 181 AGSVEQTPKKPGLRRROT 198

DB 181 AGSVEQTPKKPGLRRROT 198

RESULT 4

AAV00768

ID AAY00768 standard; Protein: 198 AA.

XX AC AAY00768;

XX 14-MAY-1999 (first entry)

XX CKI/KIP protein p27.

XX CKI/KIP protein; p27 protein; cyclin kinase inhibitor; cancer;

XX hyperproliferative disorder

XX Homo sapiens.

XX W09904238-A2.

XX 28-JAN-1999.

XX 14-JUL-1998; 98WO-US14566.

XX 15-JUL-1997; 97US-0943274

XX (DEAC-) DEACONESS HOSPITAL.

XX (MITO-) MITOTIX INC.

XX Draetta G, Loda M, Pagano M, Rolfe M;

XX WPI; 1999-132426/11.

XX N-PSDB; AAX21817

PT Methods for diagnosis and prognosis of hyperproliferative disorders

PT - by determining the level of cyclin kinase inhibitor protein(s),

XX particularly p27

XX Claim 18; Page 36 37; 53pp; English.

XX This sequence is the cyclin kinase inhibitor (CKI) protein p27. The

CC invention relates to a method for diagnosing a hyperproliferative

CC disorder, associated with the destabilisation of a CKI protein in cells

CC of a patient, comprises: (i) ascertaining the CKI protein level in a

CC sample of patient cells; and (ii) diagnosing the presence or absence of a

CC hyperproliferative disorder by utilising the ascertained CKI protein

CC level, where a reduced CKI protein level, relative to a normal control

CC cell sample, correlates with the presence of a hyperproliferative

CC disorder. The methods are useful for diagnosing disorders associated with

CC hyperproliferation, evaluating their aggressiveness and/or rate of

CC recurrence and as prognosis for evaluating a cancer patient's risk of

CC death. From the observations, treatment can be applied on the basis of

CC the patient's risk of death and/or recurrence of the cancer. The

CC diagnostic methods may also be employed as follow-up to treatment,

CC e.g. quantitation of the level of p27 protein may be indicative of the

CC effectiveness of current or previously employed cancer therapies as well

CC as the effect of these therapies upon patient prognosis. The methods and

CC reagents allow the detection of loss of p27 protein from a cell in order

CC to diagnose and phenotype proliferative disorders arising from

CC tumorigenic transformation of cells, or other hyperplastic or neoplastic

CC transformation processes as well as differentiative disorders such as

CC degeneration of tissue e.g. neurodegeneration.

XX SQ Sequence 198 AA;

Query Match 100.0%; Score 1064; DB 20; Length 198;

Best Local Similarity 100.0%; Pred. No. 7.2e-100;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSNVVSGSPSLERMDARQAEHPKPSACRNLFPGVDHEELTRDLEKHCRDMEASQKWK 60

DB 1 MSNVVSGSPSLERMDARQAEHPKPSACRNLFPGVDHEELTRDLEKHCRDMEASQKWK 60

QY 61 NFDQNHKPLEGKYEWQVEKGSIPFFYYPPPPPKGACKVPAQESQDVSGSPFAAPLIG 120

DB 61 NFDQNHKPLEGKYEWQVEKGSIPFFYYPPPPPKGACKVPAQESQDVSGSPFAAPLIG 120

QY 121 APANSEDLHLVDPKTDPSDSQTGLAEQACAGIRKRPATDDSSSTONKRANRTEENVSDGSPN 180

DB 121 APANSEDLHLVDPKTDPSDSQTGLAEQACAGIRKRPATDDSSSTONKRANRTEENVSDGSPN 180

QY 181 AGSVEQTPKKPGLRRROT 198

DB 181 AGSVEQTPKKPGLRRROT 198

RESULT 5

AAV97523

ID AAY97523 standard; Protein: 198 AA.

XX AC AAY97523;

XX 15-JAN-2001 (first entry)

XX Human p27 protein sequence.

XX Human; chimeric cyclin dependent kinase inhibitor; CDK1; therapy;

XX adenovirus E4 protein; neoplasia, p27 protein.

XX Homo sapiens.

XX W0200052184-A1.

XX 08-SEP-2000.

XX 01-MAR-2000; 2000WO-US05350.

XX The invention relates to methods of altering the polypeptide levels in a
 CC cell, using proteins selected from S-phase kinase associated proteins 1
 CC and 2 (SKP1, SKP2), SKP2 like proteins (2F) and CUL-1 (a member of the
 CC cullin/ CDC53 family of proteins). The method is useful for altering the
 CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
 CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
 CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents
 CC that modulate interactions between SKP and target proteins are useful for
 CC treating tumours.

SQ Sequence 198 AA.
 Query Match 100.0%, Score 1064, DB 22, Length 198;
 Best Local Similarity 100.0%, Pred. No. 7.2e-100;
 Matches 198; Conservative 0, Mismatches 0, Indels 0, Gaps 0.
 QY 1 MSNVRVNSGSPSLERMDARQAFHPKPSACRNIPFVDRHFFITFLEKHPFMEESQPKW 60
 DB 1 MSNVRVNSGSPSLERMDARQAFHPKPSACRNIPFVDRHFFITFLEKHPFMEESQPKW 60
 C 61 NFEQNHKPLEGRYEWQVEKGSLSPEFYYPFPKPKACVFAESQVSGSREAAFLIG 120
 DB 61 NFEQNHKPLEGRYEWQVEKGSLSPEFYYPFPKPKACVFAESQVSGSREAAFLIG 120
 QY 121 APANSEDTHLVDPKTPSDSQTGLAEQACGIRKRPATDSSSTONKRANRTEENVSDGSPN 180
 DB 121 APANSEDTHLVDPKTPSDSQTGLAEQACGIRKRPATDSSSTONKRANRTEENVSDGSPN 180
 QY 181 AGSVEQTPKKPLRRROT 198
 DB 181 AGSVEQTPKKPLRRROT 198

RESULT 11
 AAB47880
 ID AAB47880 standard; protein; 198 AA.
 AC AAB47880;
 XX 02-MAY-2002 (first entry)
 DE p27-Kip1.
 KW Cell cycle inhibitor; antisense; inner ear; sensory hair cell;
 KW support cell; auditory function; hearing disorder;
 KW sensory neuronal hearing loss; SNHL.
 OS Homo sapiens.
 XX W020294605 A2.
 XX 17-JAN 2002.
 XX 10-JUL-2001; 2001WC-0521793.
 XX 11-JUL-2000; 2000MS-0614099.
 XX (OT03-) OT03GENE USA INC.
 PA (OT03-) OT03GENE AG.
 XX Kil J, Gu R, Grigour C, Lowenheim H;
 XX W01: 2002-171713/22.
 DR N-PSDB: AAI72396.
 XX Stimulating the formation of inner ear sensory hair cells, useful for
 PT treating hearing disorder involves damaging first inner ear sensory
 PT hair cells and promoting the formation of new sensory hair cells from
 PT inner ear support cells -
 XX Disclosure: Page 64: 77pp; English.

CC The sequences given in AAB47879-85 are cell cycle inhibitors. The nucleic
 CC acids encoding these proteins may be hybridised by antisense molecules in
 CC the method of the invention. The method is for stimulating the formation
 CC of an inner ear sensory hair cell from an inner ear support cell and
 CC involves damaging a first inner ear sensory hair cell under conditions
 CC that promote the formation of at least one inner ear sensory hair cell
 CC that is in contact with the damaged first inner ear hair cell.
 CC The method is useful for stimulating the formation of inner ear
 CC cells e.g. sensory hair cells and support cells, for improving an
 CC auditory function in an inner ear, in the treatment of hearing disorder
 CC e.g. sensory neuronal hearing loss (SNHL), to identify genes and/or
 CC proteins that are capable of stimulating the formation of inner ear
 CC sensory hair cells and/or the formation of inner ear support cells
 CC from sensory hair cells. The method damages and/or kills the inner
 CC ear sensory cells, such as sensory hair cells and support cells, which
 CC results in the increased stimulation in the formation of new, inner ear
 CC hair cells, thus resulting in the improved curing of the auditory
 CC function.
 XX SQ Sequence 198 AA;

Query Match 100.0%, Score 1064, DB 23, Length 198;
 Best Local Similarity 100.0%, Pred. No. 7.2e-100;
 Matches 198; Conservative 0, Mismatches 0, Indels 0, Gaps 0;
 QY 1 MSNVRVNSGSPSLERMDARQAFHPKPSACRNIPFVDRHFFITFLEKHPFMEESQPKW 60
 DB 1 MSNVRVNSGSPSLERMDARQAFHPKPSACRNIPFVDRHFFITFLEKHPFMEESQPKW 60
 QY 61 NFEQNHKPLEGRYEWQVEKGSLSPEFYYPFPKPKACVFAESQVSGSREAAFLIG 120
 DB 61 NFEQNHKPLEGRYEWQVEKGSLSPEFYYPFPKPKACVFAESQVSGSREAAFLIG 120
 QY 121 APANSEDTHLVDPKTPSDSQTGLAEQACGIRKRPATDSSSTONKRANRTEENVSDGSPN 180
 DB 121 APANSEDTHLVDPKTPSDSQTGLAEQACGIRKRPATDSSSTONKRANRTEENVSDGSPN 180
 QY 181 AGSVEQTPKKPLRRROT 198
 DB 181 AGSVEQTPKKPLRRROT 198

RESULT 12
 AAY70307
 ID AAY70307 standard; protein; 198 AA.
 AC AAY70307;
 XX 06-JUN-2000 (first entry)
 DE Human mutant cyclin-dependent kinase inhibitor (CKI), p27 S10A protein.
 XX Cyclin-dependent kinase inhibitor; CKI; p27; human; mutant; G1 phase;
 KW KIS; serine/threonine kinase; cell proliferation; modulator; treatment;
 KW cell proliferative disease, vascular disorder, gene therapy; restenosis;
 KW atherosclerosis.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Misc-difference 10 /note= "wild type Ser substituted with Ala"
 FT W0200011165-A1.
 XX 02-MAR-2000.
 XX 20-AUG-1999; W000-0518403.
 XX 21-AUG-1998; 9808-0697710
 XX (NABE/) NABEL G J.
 PA (NABE/) NABEL E G.

KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
 KW intracellular; transcellular; transcytosis; vascular wound repair; hair;
 KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
 KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
 KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
 KW tachycardia; human; p27; p16.

XX Homo sapiens.

XX W0956540-A2.

XX 11-FEB-1999.

XX 29-JUL-1998; 98WO-US15759.

XX 29-JUL-1997; 97US-0902572.

XX (MITO-) MITOTIX INC.

XX Beach DH, Gyuris J, Lamphere L;

XX WPI: 1999-153770/13.

XX N-PSDB: AAX26229.

XX Fusion and chimeric proteins including cyclin-dependent kinase
 binding motif - used for regulation of cell proliferation and
 differentiation, for treatment of, e.g. vascular injury, cancers,
 PT fibrosis and neurodegeneration

XX Claim 63: Page 70-72; 88pp; English.

XX The invention relates to novel inhibitors of cyclin-dependent kinases
 (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
 transfection system (A) that comprises: (i) first gene construct
 comprising a sequence encoding an inhibitory polypeptide containing at
 least one CDK-binding motif for binding and inhibiting activity of a CDK,
 CC linked to a transcription regulator functional in eukaryotic cells; (ii)
 CC second gene construct comprising a sequence encoding a polypeptide that
 CC promotes endothelialisation; and (iii) a gene delivery composition for
 CC delivering the GEs to a cell for transfection. Also provided are nucleic
 CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
 CC polypeptide sequence (IP) from an intracellular protein that alters a
 CC cellular process when FP enters the cell; and (ii) a transcellular
 CC polypeptide sequence (ICP) that promotes transcytosis of FP. The FP
 CC consists of at least one CDK-binding motif and a TCP. (A) are used to
 CC treat vascular wounds that involve a break in the endothelium and
 CC excessive proliferation of smooth muscle, particularly restenosis but
 CC more generally any repair of cardiovascular damage, arteriosclerotic
 CC lesions or for endothelialisation of synthetic vascular grafts. More
 CC generally, FP are used to treat unwanted cellular proliferation in a very
 CC wide range of situations, e.g. for treating vascular diseases as above;
 CC fibrotic disorders (e.g. rheumatoid arthritis, diabetes, cirrhosis); many
 CC tumours (gliomas, leukemias); chronic inflammation; neurodegeneration;
 CC acne; also to control hair growth (e.g. to prevent hair loss caused by
 CC chemotherapy or radiation); periodontal disease; to treat tachycardia;
 CC to inhibit spermatogenesis etc. Chimeric proteins comprising CDK-binding
 CC motifs from two or more different proteins bind to CDKs so inhibit cell
 CC cycle progression, particularly smooth muscle cell proliferation. The
 CC gene constructs may also be used to produce FP in cell cultures, for
 CC production or for regulating cell differentiation in vitro. The present
 CC sequence represents a human p27-p16 fusion protein.

XX Sequence 391 AA;

Query Match 99.5%; Score 1059; DB 20; Length 391;

Best Local Similarity 100.0%; Pred. No. 5.7e-99;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SNRVNSNGSPSLERMDAPQAFHPKPSA*CNLFPGVDVHEELTPDLEKHCHMEASQPKWN 61

DB 8 SNRVNSNGSPSLERMDAPQAFHPKPSA*CNLFPGVDVHEELTPDLEKHCHMEASQPKWN 67

QY 62 FDFQNHKPLEGKYEWQVEKGSILPPFYRPPPKGACKVPAQESQVSSSRPAAPLIGA 121

DB 68 FDFQNHKPLEGKYEWQVEKGSILPPFYRPPPKGACKVPAQESQVSSSRPAAPLIGA 127

QY 122 PANSETHIVDPKTPDSQSLGLAEVCA*IPKPKPATDSDSTANKANPTEENVSDGSPNA 181

DB 128 PANSETHIVDPKTPDSQSLGLAEVCA*IPKPKPATDSDSTANKANPTEENVSDGSPNA 187

QY 182 GSVEQTPKKPLPRROT 198

DB 188 GSVEQTPKKPLPRROT 204

RESULT 15

AA97526

ID AAY97526 standard; Protein; 391 AA.

XX AC AAY97526;

XX 15-JAN-2001 (first entry)

XX Human W3 protein sequence.

XX Human, chimeric cyclin dependent kinase inhibitor, CDK1; therapy;

XX adenovirus E4 protein; neoplasia; W3 protein.

XX Homo sapiens.

XX W0200052184-A1.

XX 08-SEP-2000.

XX 01-MAK-2000; 2000WO-US05350.

XX 01-MAP-1999; 99US-0122974.

XX 08-APR-1999; 99US-0128271.

XX 09-APR-1999; 99US-0128515.

XX (CELL-) CELL GENESYS INC.

XX (MITO-) MITOTIX INC.

XX Patel S, McArthur J, Gyuris J, Mendez MJ, Finan M,

XX WPI: 2000-587315/55.

XX N-PSDB: AAA90923.

XX Protein and nucleic acid compositions for preventing and treating
 neoplasias (particularly cancer), comprises a novel chimeric cyclin
 dependent kinase inhibitor and adenovirus E4 protein -

Example 1; page 108-109; 126pp; English.

XX This sequence represents the human W3 protein
 CC the invention relates to a protein composition comprising a novel
 CC purified chimeric cyclin dependent kinase inhibitor (CDKi) and a
 CC or the DNA encoding it are useful for treating neoplasias in animals. The
 CC compositions also find use in assays to eliminate a specific
 CC sub-population of cultured cells, to determine the susceptibility of
 CC neoplastic cells to treatment with the compositions and also in assays to
 CC synchronise cell growth in cultured cells.

XX Sequence 391 AA;

Query Match 99.5%; Score 1059; DB 21; Length 391;

Best Local Similarity 100.0%; Pred. No. 5.7e-99;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SNRVNSNGSPSLERMDAPQAFHPKPSA*CNLFPGVDVHEELTPDLEKHCHMEASQPKWN 61

DB 8 SNRVNSNGSPSLERMDAPQAFHPKPSA*CNLFPGVDVHEELTPDLEKHCHMEASQPKWN 67

QY 62 FDFQNHKPLEGKYEWQVEKGSILPPFYRPPPKGACKVPAQESQVSSSRPAAPLIGA 121

GenPro version 5.1.5

Copyright (c) 1993 - 2003 Compugen Ltd

OM protein - protein search, using sw model

Run on: May 30, 2003 08:55:37 - Search time 14.8172 seconds
(without alignments)
392 644 Million full updates/sec

Title: US-09-865-018b-2

Perfect score: 1054

Sequence: 1 MSNVFVNSGSPSLERMDAFAAEHFKPSA:PNLFSPVHHEHETVDELEKHCHKDMEEASQKRW 60

Scoring table: RUSUM62

Gap: 10 6 0 Gapext 0 5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 260000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA.*
- /cgn26/ptdata/1/1aa/5A_10MB.ppt.*
- /cgn26/ptdata/1/1aa/5B_10MB.ppt.*
- /cgn26/ptdata/1/1aa/6A_10MB.ppt.*
- /cgn26/ptdata/1/1aa/6B_10MB.ppt.*
- /cgn26/ptdata/1/1aa/6C_10MB.ppt.*
- /cgn26/ptdata/1/1aa/6D_10MB.ppt.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1064	100.0	198	1	US-08-406-248-4
2	1064	100.0	198	4	US-08-847-333A-2
3	1064	100.0	198	4	US-09-240-006-6
4	1064	100.0	198	4	US-08-794-002-2
5	1064	100.0	198	4	US-09-457-568-24
6	1064	100.0	198	4	US-08-457-568-24
7	1059	99.5	391	1	US-08-580-981-2
8	1059	99.5	391	4	US-09-457-568-4
9	1059	99.5	391	4	US-09-457-646-4
10	1057	99.3	198	1	US-08-275-983B-3
11	1054	99.1	365	4	US-08-457-568-10
12	1054	99.1	365	4	US-08-457-646-10
13	1054	99.1	380	4	US-09-457-568-8
14	1054	99.1	380	4	US-09-457-646-8
15	1052	98.5	158	4	US-08-454-036-2
16	1047	98.4	365	4	US-09-457-568-6
17	1047	98.4	365	4	US-09-457-646-6
18	933	87.7	197	3	US-08-415-655-6
19	931	87.5	197	3	US-08-275-983B-2
20	931	87.5	197	4	US-09-240-006-8
21	931	87.5	197	4	US-09-415-421-57
22	931	87.5	197	4	US-08-794-002-4
23	928	87.2	147	4	US-08-854-034R-4
24	908	85.3	334	4	US-09-457-568-16
25	908	85.3	334	4	US-09-457-646-16
26	906.5	85.2	348	4	US-09-457-568-14
27	906.5	85.2	348	4	US-09-457-646-14

28	900.5	84.6	195	4	US-08-215-221-54
29	900	84.6	177	4	US-09-457-568-12
30	900	84.6	177	4	US-09-457-646-12
31	895	84.2	212	4	US-09-215-221-43
32	885	83.2	194	4	US-09-215-221-52
33	884	83.1	194	4	US-09-215-221-53
34	874	82.1	194	4	US-09-215-221-51
35	870	81.8	178	4	US-08-794-002-6
36	870	81.8	178	4	US-08-854-034R-6
37	870	81.8	198	4	US-08-275-983B-1
38	870	81.8	198	4	US-08-794-002-22
39	837	78.7	180	4	US-09-215-221-55
40	833	78.3	180	4	US-09-215-221-50
41	834	78.4	135	4	US-09-215-221-56
42	404	38.0	323	4	US-09-457-646-30
43	403	37.9	247	4	US-08-457-568-20
44	403	37.9	237	4	US-09-457-646-20
45	401	37.7	252	4	US-09-457-568-22

ALIGNMENTS

RESULT 1
US-08-406-248-4
Sequence 4, Application US/08406248
Patent No. 5736318
GENERAL INFORMATION:
APPLICANT: Mungler, Karl
APPLICANT: Jones, D. Leanne
TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING
TITLE OF INVENTION: TRANSFORMED CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ann-Louise Kermer, Ph.D., Lappin & Kusmer
STREET: 200 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,248
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: McDaniels, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: HAZ-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: amino acid
FEATURES:
MOLECULE TYPE: protein
US-08-406-248-4

Query Match	100.0%	Score 1064;	DB 1;	Length 198;
Best local Similarity	100.0%	Prod No 2 1e-103;		
Matches 198;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MSNVFVNSGSPSLERMDAFAAEHFKPSA:PNLFSPVHHEHETVDELEKHCHKDMEEASQKRW 60		
Db	1	MSNVFVNSGSPSLERMDAFAAEHFKPSA:PNLFSPVHHEHETVDELEKHCHKDMEEASQKRW 60		
Qy	61	NFDGNHKLPLEGKYEVEKSGSLPEFYFRPPKCKACKVPAQESQDYSGRSPAALIG 120		

Db 61 NFDQNHKPLEGKYEWQEVKSGSLPEFYRPPPKGACKVPAQESQDVSGSRPAAPLIG 120
QY 121 APANSEDLHLVDPKTPDSUSQTGLAQCAQIRKRPATDSSSTONKRNKTEENVSDGSPN 180
Db 121 APANSEDLHLVDPKTPDSUSQTGLAQCAQIRKRPATDSSSTONKRNKTEENVSDGSPN 180
QY 181 AGSVEQTPKKPLRRPQT 198
Db 181 AGSVEQTPKKPLRRPQT 198

RESULT 5

US-09-457-568-26
Sequence 26, Application US/09457568
Patent No. 6413943
GENERAL INFORMATION:
APPLICANT: McArthur, James G
APPLICANT: Gyuris, Jeno
TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of Smooth Muscle Cells
FILE REFERENCE: 106482.691
CURRENT APPLICATION NUMBER: US/09/457,568
CURRENT FILING DATE: 1999-12-09
EARLIER APPLICATION NUMBER: 60/122,974
EARLIER FILING DATE: 1999-03-01
EARLIER APPLICATION NUMBER: 60/153,682
EARLIER FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 26
LENGTH: 198
TYPE: PRT
ORGANISM: Homo sapiens
US-09-457-568-26

Query Match 100.0%; Score 1064; DB 4; Length 198;
Best Local Similarity 100.0%; Pred No 2 1e-103;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSNVVYVSGSPSLERMDARQAEHPKPSACRNLFPGVDHEELTRDLEKHCRDMEASQKWK 60
Db 1 MSNVVYVSGSPSLERMDARQAEHPKPSACRNLFPGVDHEELTRDLEKHCRDMEASQKWK 60
QY 61 NFDQNHKPLEGKYEWQEVKSGSLPEFYRPPPKGACKVPAQESQDVSGSRPAAPLIG 120
Db 61 NFDQNHKPLEGKYEWQEVKSGSLPEFYRPPPKGACKVPAQESQDVSGSRPAAPLIG 120
QY 121 APANSEDLHLVDPKTPDSUSQTGLAQCAQIRKRPATDSSSTONKRNKTEENVSDGSPN 180
Db 121 APANSEDLHLVDPKTPDSUSQTGLAQCAQIRKRPATDSSSTONKRNKTEENVSDGSPN 180
QY 181 AGSVEQTPKKPLRRPQT 198
Db 181 AGSVEQTPKKPLRRPQT 198

RESULT 6

US-09-457-646-26
Sequence 26, Application US/09457646
Patent No. 6420345
GENERAL INFORMATION:
APPLICANT: Patel, Salil P
APPLICANT: McArthur, James G
APPLICANT: Gyuris, Jeno
TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of Smooth Muscle Cells
FILE REFERENCE: 106482.287
CURRENT APPLICATION NUMBER: US/09/457,646
CURRENT FILING DATE: 1999-12-09
EARLIER APPLICATION NUMBER: 60/122,974
EARLIER FILING DATE: 1999-03-01

EARLIER APPLICATION NUMBER: 60/163,682
EARLIER FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patent In Ver 2.0
SEQ ID NO 26
LENGTH: 198
TYPE: PRT
ORGANISM: Homo sapiens
US-09-457-646-26

Query Match 100.0%; Score 1064; DB 4; Length 198;
Best Local Similarity 100.0%; Pred No 2 1e-103;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSNVVYVSGSPSLERMDARQAEHPKPSACRNLFPGVDHEELTRDLEKHCRDMEASQKWK 60
Db 1 MSNVVYVSGSPSLERMDARQAEHPKPSACRNLFPGVDHEELTRDLEKHCRDMEASQKWK 60
QY 61 NFDQNHKPLEGKYEWQEVKSGSLPEFYRPPPKGACKVPAQESQDVSGSRPAAPLIG 120
Db 61 NFDQNHKPLEGKYEWQEVKSGSLPEFYRPPPKGACKVPAQESQDVSGSRPAAPLIG 120
QY 121 APANSEDLHLVDPKTPDSUSQTGLAQCAQIRKRPATDSSSTONKRNKTEENVSDGSPN 180
Db 121 APANSEDLHLVDPKTPDSUSQTGLAQCAQIRKRPATDSSSTONKRNKTEENVSDGSPN 180
QY 181 AGSVEQTPKKPLRRPQT 198
Db 181 AGSVEQTPKKPLRRPQT 198

RESULT 7

US-08-589-981-2
Sequence 2, Application US/08589981
Patent No. 5672508
GENERAL INFORMATION:
APPLICANT: Gyuris, Jeno
APPLICANT: Lamphere, Lou
APPLICANT: Beach, David H.
TITLE OF INVENTION: Inhibitors of Cell-Cycle Progression, and Uses Related Thereto
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,981
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-589-981-2


```

; REFERENCE: US/09-457-646-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-457-646-10

Query Match 99.3%, Score 1057, DB 1, Length 198;
Best Local Similarity 99.0%, Pred. No. 1, 4c-102;
Matches 196; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MSNVVNSGSLERMDAPDAEHPKPSACNLFPGVDHFEI TRLEKHCHPMEFASQKWN 60
DB 1 MSNVVNSGSLERMDAPDAEHPKPSACNLFPGVDHFEI TRLEKHCHPMEFASQKWN 60
QY 61 NFDQNHKPLEGKYEWEVEKGSUPEFYRPPKPKACKVPAGESDVSGSRPAAPLIG 120
DB 61 NFDQNHKPLEGKYEWEVEKGSUPEFYRPPKPKACKVPAGESDVSGSRPAAPLIG 120
QY 121 AFANSECTHLVDPKIDFSUSQIGLAQCAGIRKRPATIDSSQNKANKRTEENVSDGSPN 180
DB 121 AFANSECTHLVDPKIDFSUSQIGLAQCAGIRKRPATIDSSQNKANKRTEENVSDGSPN 180
QY 181 AGSVETPKPKPGI RPPQT 198
DB 181 AGSVETPKPKPGI RPPQT 198

RESULT 11
US-09-457-568-10
; Sequence 10, Application US/09457568
; Patent No. 641394
; GENERAL INFORMATION:
; APPLICANT: McArthur, James G
; APPLICANT: Gyuris, Jeno
; APPLICANT: Finer, Mitchell H
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
; TITLE OF INVENTION: Smooth Muscle Cells
; FILE REFERENCE: 106482.691
; CURRENT FILING DATE: 1999-12-09
; EARLIER FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 60/122,974
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-568-10

Query Match 99.1%, Score 1054, DB 4, Length 365;
Best Local Similarity 99.5%, Pred. No. 5, 4c-102;
Matches 196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SNVSVNSGSLERMDAPDAEHPKPSACNLFPGVDHFEI TRLEKHCHPMEFASQKWN 61
DB 169 SNVSVNSGSLERMDAPDAEHPKPSACNLFPGVDHFEI TRLEKHCHPMEFASQKWN 228
QY 62 FDFONHKLPLEGKYEWEVEKGSUPEFYRPPKPKACKVPAGESDVSGSRPAAPLIG 121
DB 229 FDFONHKLPLEGKYEWEVEKGSUPEFYRPPKPKACKVPAGESDVSGSRPAAPLIG 288
QY 122 PANSEDTHLVDPKIDFSUSQIGLAQCAGIRKRPATIDSSQNKANKRTEENVSDGSPN 181
DB 289 PANSEDTHLVDPKIDFSUSQIGLAQCAGIRKRPATIDSSQNKANKRTEENVSDGSPN 348
QY 182 GSVETPKPKPGI RPPQT 198
DB 349 GSVETPKPKPGI RPPQT 465

RESULT 13
US-09-457-568-8
; Sequence 8, Application US/09457568
; Patent No. 641394
; GENERAL INFORMATION:
; APPLICANT: McArthur, James G
; APPLICANT: Gyuris, Jeno
; APPLICANT: Finer, Mitchell H
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
; TITLE OF INVENTION: Smooth Muscle Cells
; FILE REFERENCE: 106482.691
; CURRENT FILING DATE: 1999-12-09
; EARLIER FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 60/122,974
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8

; REFERENCE: US/09-457-646-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-275-983B-3

Query Match 99.3%, Score 1057, DB 1, Length 198;
Best Local Similarity 99.0%, Pred. No. 1, 4c-102;
Matches 196; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MSNVVNSGSLERMDAPDAEHPKPSACNLFPGVDHFEI TRLEKHCHPMEFASQKWN 60
DB 1 MSNVVNSGSLERMDAPDAEHPKPSACNLFPGVDHFEI TRLEKHCHPMEFASQKWN 60
QY 61 NFDQNHKPLEGKYEWEVEKGSUPEFYRPPKPKACKVPAGESDVSGSRPAAPLIG 120
DB 61 NFDQNHKPLEGKYEWEVEKGSUPEFYRPPKPKACKVPAGESDVSGSRPAAPLIG 120
QY 121 AFANSECTHLVDPKIDFSUSQIGLAQCAGIRKRPATIDSSQNKANKRTEENVSDGSPN 180
DB 121 AFANSECTHLVDPKIDFSUSQIGLAQCAGIRKRPATIDSSQNKANKRTEENVSDGSPN 180
QY 181 AGSVETPKPKPGI RPPQT 198
DB 181 AGSVETPKPKPGI RPPQT 198

RESULT 11
US-09-457-568-10
; Sequence 10, Application US/09457568
; Patent No. 641394
; GENERAL INFORMATION:
; APPLICANT: McArthur, James G
; APPLICANT: Gyuris, Jeno
; APPLICANT: Finer, Mitchell H
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
; TITLE OF INVENTION: Smooth Muscle Cells
; FILE REFERENCE: 106482.691
; CURRENT FILING DATE: 1999-12-09
; EARLIER FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 60/122,974
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-568-10

Query Match 99.1%, Score 1054, DB 4, Length 365;
Best Local Similarity 99.5%, Pred. No. 5, 4c-102;
Matches 196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SNVSVNSGSLERMDAPDAEHPKPSACNLFPGVDHFEI TRLEKHCHPMEFASQKWN 61
DB 169 SNVSVNSGSLERMDAPDAEHPKPSACNLFPGVDHFEI TRLEKHCHPMEFASQKWN 228
QY 62 FDFONHKLPLEGKYEWEVEKGSUPEFYRPPKPKACKVPAGESDVSGSRPAAPLIG 121
DB 229 FDFONHKLPLEGKYEWEVEKGSUPEFYRPPKPKACKVPAGESDVSGSRPAAPLIG 288
QY 122 PANSEDTHLVDPKIDFSUSQIGLAQCAGIRKRPATIDSSQNKANKRTEENVSDGSPN 181
DB 289 PANSEDTHLVDPKIDFSUSQIGLAQCAGIRKRPATIDSSQNKANKRTEENVSDGSPN 348
QY 182 GSVETPKPKPGI RPPQT 198
DB 349 GSVETPKPKPGI RPPQT 465
```

LENGTH: 480

TYPE: P81

ORGANISM: Homo sapiens

US-09-457-646-B

Query Match: 99.9% Score: 1054; ID: 4; Length: 480;

Best Local Similarity: 99.9% Prod. No. 5,7e-102;

Matches: 196; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;

Q7 2 SRVYVNSGPTFMAGVAPRRTSAENLQVIHELLKGRKRLMLKASQAWK 61

104 SRVYVNSGPTFMAGVAPRRTSAENLQVIHELLKGRKRLMLKASQAWK 104

Q7 62 FPGNQIKPDKYTKWVYVNSGPTFMAGVAPRRTSAENLQVIHELLKGRKRLMLKASQAWK 121

104 FPGNQIKPDKYTKWVYVNSGPTFMAGVAPRRTSAENLQVIHELLKGRKRLMLKASQAWK 104

Q7 244 FPGNQIKPDKYTKWVYVNSGPTFMAGVAPRRTSAENLQVIHELLKGRKRLMLKASQAWK 403

104 FPGNQIKPDKYTKWVYVNSGPTFMAGVAPRRTSAENLQVIHELLKGRKRLMLKASQAWK 104

Q7 122 FANSETHLVDKPTFPTQVQVLAQACATREKPAIDSSGUNKKRNTEENVSDGSPNA 181

104 FANSETHLVDKPTFPTQVQVLAQACATREKPAIDSSGUNKKRNTEENVSDGSPNA 104

Q7 304 FANSETHLVDKPTFPTQVQVLAQACATREKPAIDSSGUNKKRNTEENVSDGSPNA 463

104 FANSETHLVDKPTFPTQVQVLAQACATREKPAIDSSGUNKKRNTEENVSDGSPNA 104

Q7 182 GSVEQTPKKKGLRRROT 198

104 GSVEQTPKKKGLRRROT 104

Q7 464 GSVEQTPKKKGLRRROT 480

104 GSVEQTPKKKGLRRROT 104

Q7 182 GSVEQTPKKKGLRRROT 198

104 GSVEQTPKKKGLRRROT 104

Q7 464 GSVEQTPKKKGLRRROT 480

104 GSVEQTPKKKGLRRROT 104

Q7 182 GSVEQTPKKKGLRRROT 198

104 GSVEQTPKKKGLRRROT 104

Q7 464 GSVEQTPKKKGLRRROT 480

104 GSVEQTPKKKGLRRROT 104

Q7 182 GSVEQTPKKKGLRRROT 198

104 GSVEQTPKKKGLRRROT 104

Q7 464 GSVEQTPKKKGLRRROT 480

104 GSVEQTPKKKGLRRROT 104

Q7 182 GSVEQTPKKKGLRRROT 198

104 GSVEQTPKKKGLRRROT 104

Q7 464 GSVEQTPKKKGLRRROT 480

104 GSVEQTPKKKGLRRROT 104

Q7 182 GSVEQTPKKKGLRRROT 198

104 GSVEQTPKKKGLRRROT 104

Q7 464 GSVEQTPKKKGLRRROT 480

104 GSVEQTPKKKGLRRROT 104

Q7 182 GSVEQTPKKKGLRRROT 198

104 GSVEQTPKKKGLRRROT 104

Q7 464 GSVEQTPKKKGLRRROT 480

104 GSVEQTPKKKGLRRROT 104

Q7 182 GSVEQTPKKKGLRRROT 198

104 GSVEQTPKKKGLRRROT 104

Q7 464 GSVEQTPKKKGLRRROT 480

104 GSVEQTPKKKGLRRROT 104

Q7 182 GSVEQTPKKKGLRRROT 198

104 GSVEQTPKKKGLRRROT 104

Q7 464 GSVEQTPKKKGLRRROT 480

104 GSVEQTPKKKGLRRROT 104

Q7 182 GSVEQTPKKKGLRRROT 198

104 GSVEQTPKKKGLRRROT 104

Q7 464 GSVEQTPKKKGLRRROT 480

104 GSVEQTPKKKGLRRROT 104

Q7 182 GSVEQTPKKKGLRRROT 198

104 GSVEQTPKKKGLRRROT 104

Q7 464 GSVEQTPKKKGLRRROT 480

104 GSVEQTPKKKGLRRROT 104

Q7 182 GSVEQTPKKKGLRRROT 198

104 GSVEQTPKKKGLRRROT 104

Q7 464 GSVEQTPKKKGLRRROT 480

104 GSVEQTPKKKGLRRROT 104

Q7 182 GSVEQTPKKKGLRRROT 198

104 GSVEQTPKKKGLRRROT 104

Q7 464 GSVEQTPKKKGLRRROT 480

104 GSVEQTPKKKGLRRROT 104

Q7 182 GSVEQTPKKKGLRRROT 198

104 GSVEQTPKKKGLRRROT 104

Q7 464 GSVEQTPKKKGLRRROT 480

104 GSVEQTPKKKGLRRROT 104

US-09-865-018b-2

Sequence 2: Application US/08640-000

Patent No. 6,057,774

GENERAL INFORMATION:

APPLICANT: MASSACHUSETTS, JOHN M.

APPLICANT: ROBERTS, JAMES M.

APPLICANT: KOTLI, ANDREW

APPLICANT: POLYAK, KORNELIA

TITLE OF INVENTION: ISOLATED P21 PROTEIN AND METHOD FOR ITS

USE IN TREATING CANCER

NUMBER OF SEQUENCES: 27

CURRENT INVENTOR ADDRESS:

ADDRESSEE: POLY, HOWE & ELLIOTT LLP

STREET: ONE POST OFFICE SQUARE

CITY: BOSTON

STATE: MA

COUNTRY: USA

DATE: 02/09/2000

COMPUTER REPEATABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: SYSTEM 3.5.2/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 05/08/954,030A

FILING DATE: 09 MAY 1997

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 46,709

REFERENCE/INVENTOR NUMBER: MIV 079,004

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-842-1000

TELEFAX: 617-842-7000

INFORMATION FOR SEQ ID NOS: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 98 amino acids

TYPE: amino acid

FEATURES: 11964

MOLECULE TYPE: protein

US-09-865-018b-2

Query Match

Best Local Similarity: 99.9% Score: 1054; ID: 4; Length: 480;

Matches: 196; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;

Q7 2 SRVYVNSGPTFMAGVAPRRTSAENLQVIHELLKGRKRLMLKASQAWK 61

104 SRVYVNSGPTFMAGVAPRRTSAENLQVIHELLKGRKRLMLKASQAWK 104

Q7 62 FPGNQIKPDKYTKWVYVNSGPTFMAGVAPRRTSAENLQVIHELLKGRKRLMLKASQAWK 121

104 FPGNQIKPDKYTKWVYVNSGPTFMAGVAPRRTSAENLQVIHELLKGRKRLMLKASQAWK 104

Q7 244 FPGNQIKPDKYTKWVYVNSGPTFMAGVAPRRTSAENLQVIHELLKGRKRLMLKASQAWK 403

104 FPGNQIKPDKYTKWVYVNSGPTFMAGVAPRRTSAENLQVIHELLKGRKRLMLKASQAWK 104

Q7 122 FANSETHLVDKPTFPTQVQVLAQACATREKPAIDSSGUNKKRNTEENVSDGSPNA 181

104 FANSETHLVDKPTFPTQVQVLAQACATREKPAIDSSGUNKKRNTEENVSDGSPNA 104

Q7 304 FANSETHLVDKPTFPTQVQVLAQACATREKPAIDSSGUNKKRNTEENVSDGSPNA 463

104 FANSETHLVDKPTFPTQVQVLAQACATREKPAIDSSGUNKKRNTEENVSDGSPNA 104

Q7 182 GSVEQTPKKKGLRRROT 198

104 GSVEQTPKKKGLRRROT 104

Q7 464 GSVEQTPKKKGLRRROT 480

104 GSVEQTPKKKGLRRROT 104

Q7 182 GSVEQTPKKKGLRRROT 198

104 GSVEQTPKKKGLRRROT 104

Q7 464 GSVEQTPKKKGLRRROT 480

104 GSVEQTPKKKGLRRROT 104

Q7 182 GSVEQTPKKKGLRRROT 198

104 GSVEQTPKKKGLRRROT 104

Q7 464 GSVEQTPKKKGLRRROT 480

104 GSVEQTPKKKGLRRROT 104

Q7 182 GSVEQTPKKKGLRRROT 198

104 GSVEQTPKKKGLRRROT 104

Q7 464 GSVEQTPKKKGLRRROT 480

104 GSVEQTPKKKGLRRROT 104

Q7 182 GSVEQTPKKKGLRRROT 198

104 GSVEQTPKKKGLRRROT 104

Q7 464 GSVEQTPKKKGLRRROT 480

104 GSVEQTPKKKGLRRROT 104

Q7 182 GSVEQTPKKKGLRRROT 198

104 GSVEQTPKKKGLRRROT 104

Search completed: May 30, 2003, 09:00:44.
Job time: 15.892 sec

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd

OM protein - protein search, using sw model

Run on: May 30, 2003, 08:58:22 : search time 20.004 seconds
(without alignments)
991.756 Million cell updates/sec

Title: US-09-865-018B-2
Perfect score: 1064
Sequence: 1 MSNVVSVNSGSPSIPRMTAPG PNAQSVHQLKKKPLPPQT 108

Scoring table: BL0SUM62
Gapop 10 0 , Gapext 0 5

Searched: 383519 seqs, 10122694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /gen2/6/prodata/1/pub/paa/US08_NEW_PRR pep.*
2: /gen2/6/prodata/1/pub/paa/PCT_NEW_PRR pep.*
3: /gen2/6/prodata/1/pub/paa/US06_NEW_PRR pep.*
4: /gen2/6/prodata/1/pub/paa/US06_PRR01MB pep.*
5: /gen2/6/prodata/1/pub/paa/US07_NEW_PRR pep.*
6: /gen2/6/prodata/1/pub/paa/US07_PRR01MB pep.*
7: /gen2/6/prodata/1/pub/paa/US07_PRR02MB pep.*
8: /gen2/6/prodata/1/pub/paa/US08_PRR01MB pep.*
9: /gen2/6/prodata/1/pub/paa/US08_NEW_PRR pep.*
10: /gen2/6/prodata/1/pub/paa/US09_PRR01MB pep.*
11: /gen2/6/prodata/1/pub/paa/US10_NEW_PRR pep.*
12: /gen2/6/prodata/1/pub/paa/US10_PRR01MB pep.*
13: /gen2/6/prodata/1/pub/paa/US09_NEW_PRR pep.*
14: /gen2/6/prodata/1/pub/paa/US09_PRR01MB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1064	100.0	198	9	US-09-970-561-2
2	1059	99.5	493	8	US-08-903-572-2
3	1054	99.1	365	8	US-08-902-572-8
4	1054	99.1	380	8	US-08-902-572-6
5	1052	98.9	198	10	US-09-865-018-2
6	928	87.2	197	10	US-09-865-018-4
7	908	85.3	334	8	US-08-903-572-22
8	906.5	85.2	348	8	US-08-903-572-24
9	900	84.6	167	8	US-08-902-572-16
10	870	81.8	178	10	US-09-865-018-5
11	403	37.9	237	8	US-08-902-572-26
12	401	37.7	252	8	US-08-902-572-28
13	394	37.0	70	8	US-08-903-572-29
14	175.5	16.5	247	10	US-09-925-297-770
15	171.5	16.1	164	9	US-09-221-268-4
16	171.5	16.1	164	9	US-09-221-268-5
17	171.5	16.1	164	10	US-08-865-018-24
18	171.5	16.1	164	10	US-09-940-766-2
19	100	5.4	191	10	US-09-733-507-2

20	100	9.4	191	10	US-09-733-507-10
21	98	9.2	19	12	US-10-042-417-85
22	97	4.1	1495	4	US-10-154-668-478
23	96	4.0	1278	4	US-10-154-668-188
24	94	8.8	2665	10	US-09-864-761-34248
25	93.5	8.8	1297	9	US-09-291-417-14
26	88.5	8.3	212	10	US-09-733-507-12
27	86	8.1	1460	10	US-09-871-916-2
28	85	8.0	472	9	US-09-953-407-2
29	85	8.0	520	9	US-09-495-898A-19
30	85	8.0	1429	9	US-09-953-407-1
31	84.5	7.9	348	10	US-09-840-787-10
32	84.5	7.9	1239	9	US-10-076-622-577
33	84.5	7.9	1249	12	US-10-007-805-577
34	84	7.9	266	9	US-09-884-465A-304
35	84	7.9	888	9	US-09-884-465A-404
36	84	7.9	889	9	US-09-884-465A-348
37	84	7.9	894	9	US-09-884-465A-347
38	84	7.9	895	9	US-09-884-465A-347
39	84	7.9	900	9	US-09-884-465A-333
40	84	7.9	900	9	US-09-884-465A-334
41	84	7.9	1163	9	US-09-932-257A-3
42	83.5	7.8	1207	9	US-10-024-368-5
43	83	7.8	847	9	US-09-875-323-2
44	83	7.8	847	9	US-10-162-012-2
45	84	7.8	974	9	US-10-038-886-4

ALIGNMENTS

RESULT 1

US-09-970-561-2
: Sequence 2, Application US/09/970-561
: Publication No. US/09/02,634A1
: GENERAL INFORMATION:
: APPLICANT: Nandikar, Krishan
: APPLICANT: Yang, Mei
: TITLE OF INVENTION: p27KIP1-1-FKBP 12 Protein Complexes
: FILE REFERENCE: Pura-14 (US/09/514,000)
: CURRENT APPLICATION NUMBER: US/09/970,561
: CURRENT FILING DATE: 2001.10.03
: PRIOR APPLICATION NUMBER: PTL/US/99/13659
: PRIOR FILING DATE: 1999-06-18
: PRIOR APPLICATION NUMBER: USSN 09/719,755
: PRIOR FILING DATE: 2000-12-15
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 2
: LENGTH: 198
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-970-561-2

Query Match	100.0%	Score 1064	DB 9	Length 198
Best Local Similarity	100.0%	Prod No 2.3e84		
Matches 198	Conservative 9	Mismatches 0	Indels 0	Gaps 0
QY	1	MSNVVSVNSGSPSIPRMTAPG	PNALPSPVDFHFLTPLEKHPDMEEASQKRW	60
IR	1	MSNVVSVNSGSPSIPRMTAPG	PNALPSPVDFHFLTPLEKHPDMEEASQKRW	60
QY	1	NPFFQNHKTPGKYPVDFHFLTPLEKHPDMEEASQKRW	PNALPSPVDFHFLTPLEKHPDMEEASQKRW	120
IR	1	NPFFQNHKTPGKYPVDFHFLTPLEKHPDMEEASQKRW	PNALPSPVDFHFLTPLEKHPDMEEASQKRW	120
QY	1	APANSETHLVDFKTPGKYPVDFHFLTPLEKHPDMEEASQKRW	PNALPSPVDFHFLTPLEKHPDMEEASQKRW	180
IR	1	APANSETHLVDFKTPGKYPVDFHFLTPLEKHPDMEEASQKRW	PNALPSPVDFHFLTPLEKHPDMEEASQKRW	180
QY	1	ANSVBTPPKKPIPPQT	198	
IR	1	ANSVBTPPKKPIPPQT	198	


```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1 0, Version #1 0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 36,709
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-069.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-902-572-6
;
; Query Match 99.1%; Score 1054; DB 8; Length 380;
; Best Local Similarity 99.5%; Pred. No. 3.6e-83;
; Matches 196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Q7 2 SNRVVSNNGSPSLERMDARQAEHPKPSACPNLFPGVDHHEELTRDLEKHCGRDMEASQPKW 61
; DB 184 SNRVVSNNGSPSLERMDARQAEHPKPSACPNLFPGVDHHEELTRDLEKHCGRDMEASQPKW 243
; QY 62 EEFQNEKPLFQKYEWQVEKESLPEFYYPKPKGAKVFAESQVSGSPAAFLIG 141
; DB 244 EEFQNEKPLFQKYEWQVEKESLPEFYYPKPKGAKVFAESQVSGSPAAFLIG 303
; QY 122 FANSETHLVGPKTQPSQTLAEQACGIRKPPATDSSQNKPKANFTENVSQSPN 181
; DB 304 FANSETHLVGPKTQPSQTLAEQACGIRKPPATDSSQNKPKANFTENVSQSPN 363
; QY 182 AGSVEQTPKKPGSLPRQT 198
; DB 364 AGSVEQTPKKPGSLPRQT 390
;
; RESULT 5
; US-09-865-018-2
; Sequence 2, Application US/09865018
; Patent No. US2002010886A1
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; Roberts, James M
; Koff, Andrew
; Polyak, Kornelia
; TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS
; PRODUCTION AND USE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1 0, Version #1 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,018
; FILING DATE: 24-May-2001
; PRIOR APPLICATION DATA:
;
; US-09-865-018-4
; Sequence 4, Application US/09865018
; Patent No. US2002010886A1
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; Roberts, James M.
; Koff, Andrew
; Polyak, Kornelia
; TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS
; PRODUCTION AND USE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,018
; FILING DATE: 24-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,039
; FILING DATE: 09-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-079 04
;
; US-09-865-018-2
; Query Match 98.9%; Score 1052; DB 10; Length 198;
; Best Local Similarity 99.0%; Pred. No. 2.5e-83;
; Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; Q7 1 MSNVVSNNGSPSLERMDARQAEHPKPSACPNLFPGVDHHEELTRDLEKHCGRDMEASQPKW 60
; DB 1 MSNVVSNNGSPSLERMDARQAEHPKPSACPNLFPGVDHHEELTRDLEKHCGRDMEASQPKW 60
; QY 61 NDFQNEKPLFQKYEWQVEKESLPEFYYPKPKGAKVFAESQVSGSPAAFLIG 120
; DB 61 NDFQNEKPLFQKYEWQVEKESLPEFYYPKPKGAKVFAESQVSGSPAAFLIG 120
; QY 121 FANSETHLVGPKTQPSQTLAEQACGIRKPPATDSSQNKPKANFTENVSQSPN 180
; DB 121 FANSETHLVGPKTQPSQTLAEQACGIRKPPATDSSQNKPKANFTENVSQSPN 180
; QY 181 AGSVEQTPKKPGSLPRQT 198
; DB 181 AGSVEQTPKKPGSLPRQT 198
;
; RESULT 6
; US-09-865-018-4
; Sequence 4, Application US/09865018
; Patent No. US2002010886A1
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; Roberts, James M.
; Koff, Andrew
; Polyak, Kornelia
; TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS
; PRODUCTION AND USE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,018
; FILING DATE: 24-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,039
; FILING DATE: 09-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-079 04

```


Db 72 GYVQWQVEKSGSLPEFYVPPPPKPKGACVKVPAQESQVSGSPFAAPLIGAFANSEDTHLV 131

QY 132 DKTTPDSQSLGAEQACGKPKPATGSSSTONKPKANFTENVS... -GSNAG 182

Db 132 DKTTPDSQSLGAEQACGKPKPATGSSSTONKPKANFTENVS... -GSNAG 182

QY 183 SVE 185

Db 192 SVE 194

RESULT 9

US-08-902-572-18

Sequence 18, Application US/08902572

Patent No. US20020068706A1

GENERAL INFORMATION:

APPLICANT: Gyuris, Jenö

APPLICANT: Lamphere, Lou

APPLICANT: Beach, David H.

TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND

TITLE OF INVENTION: RELATED THEREPTO

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/902,572

FILING DATE: 23 JUL 1997

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: MIV-069,03

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-832-1000

TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 167 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-902 572 18

Query Match 84.6%, Score 900, DR 2, Length 167;

Best Local Similarity 100.0%, Pred No 2 6e-70;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SLERMLAQAEHPKPSACRNLFQVUHFELTFLGKHCIFMFFASQKWNDFGNHKKPLE 71

Db 2 SLERMLAQAEHPKPSACRNLFQVUHFELTFLGKHCIFMFFASQKWNDFGNHKKPLE 61

QY 72 GYVQWQVEKSGSLPEFYVPPPPKPKGACVKVPAQESQVSGSPFAAPLIGAFANSEDTHLV 131

Db 62 GYVQWQVEKSGSLPEFYVPPPPKPKGACVKVPAQESQVSGSPFAAPLIGAFANSEDTHLV 121

QY 132 DKTTPDSQSLGAEQACGKPKPATGSSSTONKPKANFTENVS... -GSNAG 182

Db 132 DKTTPDSQSLGAEQACGKPKPATGSSSTONKPKANFTENVS... -GSNAG 182

RESULT 10

US-09-865-018-6

Sequence 5, Application US/09865018

Patent No. US20020110886A1

GENERAL INFORMATION:

APPLICANT: Massague, Joan

APPLICANT: Roberts, James M.

APPLICANT: Koff, Andrew

APPLICANT: Polyak, Kornelia

TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS

TITLE OF INVENTION: PRODUCTION AND USE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/865,018

FILING DATE: 24-May-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/854,049

FILING DATE: 09-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: MTV-079 04

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-832-1000

TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 178 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-865-018-6

Query Match 81.8%, Score 870, DB 10; Length 178;

Best Local Similarity 91.0%, Pred. No. 1, 1e-67;

Matches 162; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MSNVVSVNSGSPSTLPRMDAQAPKPSACRNLFQVUHFELTFLGKHCIFMFFASQKWNDFGNHKKPLE 71

Db 1 MSNVVSVNSGSPSTLPRMDAQAPKPSACRNLFQVUHFELTFLGKHCIFMFFASQKWNDFGNHKKPLE 60

QY 61 NTFQNHKKPLESKYEWQVEKSGSLPEFYVPPPPKPKGACVKVPAQESQVSGSPFAAPLIG 120

Db 61 NTFQNHKKPLESKYEWQVEKSGSLPEFYVPPPPKPKGACVKVPAQESQVSGSPFAAPLIG 120

QY 121 AFANSEDTHLVFKTKTSSQVSGSLAEQACGKPKPATGSSSTONKPKANFTENVS... -GSNAG 178

Db 121 AFANSEDTHLVFKTKTSSQVSGSLAEQACGKPKPATGSSSTONKPKANFTENVS... -GSNAG 178

RESULT 11

US-08-902-572-26

Sequence 26, Application US/08902572

Patent No. US20020068706A1

GENERAL INFORMATION:

APPLICANT: Gyuris, Jenö

APPLICANT: Lamphere, Lou

APPLICANT: Beach, David H.

TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND

TITLE OF INVENTION: RELATED THEREPTO

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:


```

Query Match          37.0%, Score 394, DB 8, Length 70,
Best Local Similarity 100.0%, Pred. No. 3,76-27,
Matches 69; Conservative 0, Mismatches 0, Indels 0, Gaps 0;

25 KPSAATNIFGVVDEEETPOLERHPTMTFASQKWNFIPTLNHKPLGKYEWVEVKGSL 84
|||||
2 KPSACRNLEGVVDEEETPOLERHPTMTFASQKWNFIPTLNHKPLGKYEWVEVKGSL 61
|||||

85 PFQFYPPPP 93
|||||
62 PFQFYPPPP 79
|||||

```

```

RESULT 14
US-09 925 297 770
; Sequence 770, Affiliation US/09025297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; AFFILICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: PCT/US03/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,470
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 770
; LENGTH: 247
; TYPE: FRI
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (131)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-297-770

```

```
Query March      16.5%: Score 175.5; DB 10; Length 247;
Best Local Similarity 29.8%; Prod. No. 1:2e-07;
Matches 59; Conservative 20; Mismatches 64; Indels 55; Gaps 9;
```

	QY	3	NRVVSGSPSLRMDAQAQAEHPKPCACNLPGPVDHEELTPDLEKHCHRDMEEAASORKWF	62
	Ddb	84	HVTGWCQS-----EPMRHAKPLFGPVTSFGLSFDCTALWAGCLOAREXWNF	134
	QY	63	DFNHNHPIFKKYFWGEVGKSLIPFYYPYPPPKPAKKVPAAESQLVSSGSFPAPLIGAP	122
	Ddb	135	DFVTETPLEGDFAWRVRLGLEKLYL-----PLG----PRKGDELGGGR-----	176
	QY	123	ANSEUHI VLPKTFPSLSITGLAEACAGLRKPATU---USSILNKRNARTTEENVSDGSPN	180
	Ddb	177	-----EPRTSPALLDGTAE-----DHVTLSTLTLYPPSGEQ_AEGSPG	215
	QY	181	AGSVQEOTPKPKGLRRQT	198
	Ddb	216	GPTDSO-----GPRROT	228

```

RESULT 15
US-09-221-268-3
: Sequence 3, Application 92/05221268A
: Publication No. US20020183509A1
: GENERAL INFORMATION:
: APPLICANT: Fisher, Paul B. and
: APPLICANT: Jiang, Hongping
: APPLICANT: The Trustees of Columbia University in the City of New York
: TITLE OF INVENTION: METHOD FOR GENERATING A SUBTRACTED CDNA LIBRARY AND
: TITLE OF INVENTION: USES OF THE GENERATED LIBRARY
: FILE REFERENCE: 0575/43563-B
: CURRENT APPLICATION NUMBER: US-09-221-268A

```

```

; CURRENT FILING DATE: 1998-12-23
; EARLIER APPLICATION NUMBER: 08/316,537
; EARLIER FILING DATE: 1994-09-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 164
; TYPE: PET
; ORGANISM: MDA-6(2)
US-09-221-248-3

```

```

Query Match      16.18; Score 171.5; DB 9; Length 164.
Best Local Similarity 31.4%; Pred No 16e-07;
Matches 58; Conservative 20; Mismatches 58; Indels 49; Gaps 10;

17 LAKOAEHKPS-ACKNLKCPVDEHLEIKLEKCHKMEEASOKKNFDFQNHKPLEGKYE 75
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
7 DVPQ--NPGSKAKCPPLGPDVSEQLSPDCTALMAGCTQEAPEPNFDFVTFPLEGDA 64
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

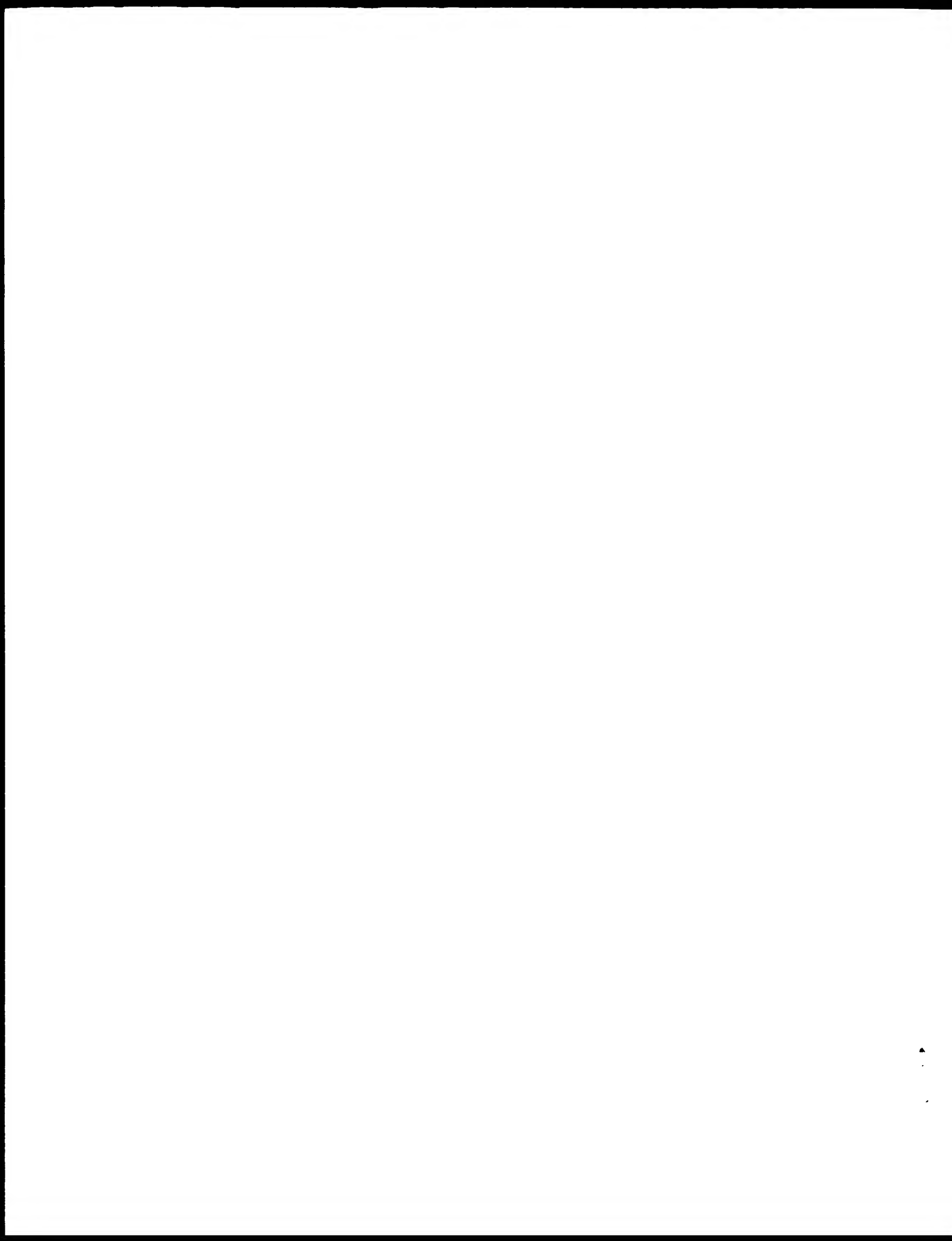
76 WQVEKGLSLPFIYYPPKPKGACKYPAQESDVSQSKRAAPLIGAPANSEDTHLVDKPT 135
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
65 WEPVPTGLPLKYL-----PTG-----PPGPPNPLGGSP-----RPGT 97
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

136 DFDSTSLTGLARWAGIIPKPPATG---DSSTLNKRNPIENVSQSGSNAGSVQIIPKKGL 193
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
98 SFALLQ-NTAEE-----DHVELSLSLTLVPFSSQV-AEGSPKPHGINSQ-----GR 140
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

194 PPRQT 198
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
141 KRRT 145
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: May 30, 2003, 09:05:09
Job time : 21.2093 secs



GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuLink Ltd

OM protein - protein search, using sw model

Run on: May 30, 2003, 06:54:42, Search time: 39.479 seconds
(without alignments)
1144,739 Million cell updates/sec

File: US-09-865-018b-2
Perfect score: 1064
Sequence: 1 MSNVVSVNCSPLFPMAPQ PNAQSVETPKKPGLPPT 198

Scoring table: BLOSUM62
Gap: 10.0, Gapext: 0.5

Searched: 28424 seqs, 961442 residues

Total number of hits satisfying chosen parameters: 28324

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Prof. X. is the author of this hit's predicted by domain database.
Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1054	99.1	198	2 152718	g-pro p27Kip1 prote
2	921	87.5	197	2 149064	cyclin-cdk inhibit
3	220.5	20.7	216	2 392424	cyclin-dependent k
4	218	20.5	210	2 151682	cyclin-dependent k
5	212.5	20.0	218	2 143263	cyclin-cdk inhibit
6	191	18.0	164	2 184725	tumor suppressor p
7	179.5	16.5	153	2 143023	tumor suppressor p
8	176.5	16.6	143	2 A49438	p53 tumor suppress
9	172.5	16.2	121	2 168674	cyclin-dependent k
10	170.5	16.0	181	2 154380	cyclin-dependent k
11	151.5	14.2	258	2 124439	hypothetical prote
12	145	11.7	184	2 124496	hypothetical prote
13	100	9.4	191	2 T01132	cyclin-dependent k
14	95	8.9	399	2 J62522	paired type homeod
15	95	8.9	735	2 S43147	alpha aducrin - ra
16	95	8.9	1173	2 T42719	TPR-containing/SH2
17	94	8.8	246	1 S49770	hypothetical prote
18	94	8.8	856	2 T16543	hypothetical prote
19	93.5	8.8	1307	2 T17453	ERG-associated pro
20	93	8.7	403	2 T47621	basic transcription
21	92	8.5	439	2 B44774	hypothetical prote
22	91.5	8.6	1076	2 S44764	C27D11.1 protein -
23	90.5	8.5	256	2 148401	histone deacetylase
24	90	8.5	913	2 B47369	translation initia
25	89	8.5	913	2 A82587	translation initia
26	89.5	8.4	515	2 T05863	hypothetical prote
27	89	8.4	611	1 S12766	translation initia
28	89	8.4	1211	2 T42230	AP4 protein - mous
29	88.5	8.3	388	1 Q69V	transforming prote

ALIGNMENTS

RESULT 1

152718

Gene p27Kip1 protein - human

C:Species: Homo sapiens (man)

C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000

C:Accession: I52718

R:Pietropoli, J.A.; Rohlander, S.K.; Sato, Y.; Papadopoulos, N.; Liu, B.; Friedman, C.

Cancer Res. 55, 1206-1210, 1995

A:Title: Assignment of the human p27Kip1 gene to 12p13 and its analysis in leukemias.

A:Reference number: I52718; MUID:95188144; PMID:7882309

A:Accession: I52718

A:Status: preliminary; translated from GB/EMBL/DDJB

A:Molecule type: DNA

A:Residues: 1-198 (RES)

A:Address references: GR S76988; NIH:3492402; PIR:AA11444.1; IID 34251944

C:Genetics:

A:Gene: p27Kip1

A:Introns: 159/1

Query Match 99.1%; Score 1054; DB 2; Length 198;

Best Local Similarity 99.0%; Pred. No. 3,1e-76;

Matches 196; Conservative 1; Mismatches 1; Indels 0; Caps 0;

QY 1 MSNVVSVNCSPLFPMAPQAFHPKPSAQNLFSPVDHEELTPGLEKHPDMEESQKWK 60

DB 1 MSNVVSVNCSPLFPMAPQAFHPKPSAQNLFSPVDHEELTPGLEKHPDMEESQKWK 60

QY 61 NPLQNHKRTPEKYPWQFVKQSLPEYYHGFHPKTAKVPAESQSWSSSHAAFLSS 120

DB 61 NPLQNHKRTPEKYPWQFVKQSLPEYYHGFHPKTAKVPAESQSWSSSHAAFLSS 120

QY 121 APANSETHLVDPKTDSPSTGTAELCAITKFFPATIOSSTNFRANFTEENVSDGSPN 180

DB 121 APANSETHLVDPKTDSPSTGTAELCAITKFFPATIOSSTNFRANFTEENVSDGSPN 180

QY 161 AGSVEQTPKKKGLPPPT 198

DB 161 AGSVEQTPKKKGLPPPT 198

RESULT 2

149064

cyclin-cdk inhibitor p27 - mouse

N:Alternative names: p27, p27, G1 cyclin-cdk-dependent kinase inhibitor p27

C:Species: Mus musculus (house mouse)

C:Date: 04-Mar-1996 #sequence_revision 04-Mar-1996 #text_change 05-Nov-1996

C:Accession: I49064

R:Toyoshima, H.; Hunter, T.

Cell 78, 67-74, 1994

A:Title: p27, a novel inhibitor of G1 cyclin-cdk protein kinase activity, is related

A:Reference number: I49064; MUID:94306519; PMID:8033213

A:Accession: I49064

QY 122 PAFSGVSSSRPAAPLIGANSEDTHLVPRKTPDSQGLAFQAGTAKKPAIG 158
 ||||| : : : : :
 Db 121 SCPPAGEADGLEAPGEP-PSAPASAVVADATFAT-----PAPASD 162
 ||||| : : : : :
 QY 156 PSSR--TQNKFRANFTIRNVSMGTHARS--VFETPKK 190
 ||||| : : : : :
 Db 163 LTSDIPEVTIVATSDPTPTDPIPDANPDVATFGEELAVPEQ 203
 ||||| : : : : :
 RESULT 6
 184725
 C:Species: Mus musculus (house mouse)
 C:Title: Topological control of p21WAF1/Cip1 expression in normal and neoplastic tissues
 C:Date: 02 Jun 1996 #sequence_revision 02 Aug 1996 #text_change 20 Jun 2000
 C:Accession: 184725
 R:El-Deiry, W.S.; Tokino, T.; Waldman, T.; Velculescu, V.; Oliner, J.D.; Burrell, M.; Hill
 Cancer Res. 55, 2910-2919, 1995
 A:Title: Topological control of p21WAF1/Cip1 expression in normal and neoplastic tissues
 A:Reference number: 149296; MUID:95316868; PMID:7796420
 A:Accession: 184725
 A:Status: preliminary; translated from GR/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-164 <RES>
 A:Cross-references: EMBL:024174; NID:9902581; FIDN:AA052221.1; FID:9902582
 C:Genetics:
 A:Gene: WAF1

Query Match 18.0%; Score 191; Db 2; Length 164;
 Best Local Similarity 29.2%; Pred. No. 3.3e-07;
 Matches 54; Conservative 16; Mismatches 67; Indels 48; Gaps 7.
 QY 17 DAAQAEHPKPSACNLFPGVDHFEITPDLEKHCRCMDMEASQPKWNFDQNHKPIPGKYEW 76
 ||||| : : : : :
 Db 6 DVPVPVPH-RSKVCRCLFGPVDSEQLSRDCDALMAGCQAEARERWPDFVTEPLEGNFVW 64
 ||||| : : : : :
 QY 77 QEVEKGSILPEFYYP---PRPPKGACKVPAQESQDVSGSRPAAPLIGANSEDTHLVDP 133
 ||||| : : : : :
 Db 65 EPVPSLSLPRKVLSPGSPSLGSGIKPPSTSSALLQGPAP----- 105
 QY 134 KTDPSDSQTGLAFOCAGTAKKPAAPLIGANSEDTSTONKPNPTEENVSGSPNAGSVQIIPKKPQL 193
 ||||| : : : : :
 Db 107 ---PRD-HVALSLSLTIVSERP-----ERPED-----SPGSGTSGTQ-----GR 140
 ||||| : : : : :
 QY 194 RRQQT 198
 ||||| : : : : :
 Db 141 RRQQT 145

RESULT 7
 149023
 tumor suppressor p21 WAF1/Cip1 [imported] - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02 Jun 1996 #sequence_revision 02 Jun 1996 #text_change 20 Jun 2000
 C:Accession: 149023; 149296
 R:Huppig, K.; Siwarski, D.; Dostik, J.; Michieli, P.; Chedid, M.; Keed, S.; Mock, B.; Givol
 Oncogene 9, 3017-3020, 1994
 A:Title: Molecular cloning, sequencing, chromosomal localization and expression of mouse
 A:Reference number: 149023; MUID:94466751; PMID:8044607
 A:Accession: 149023
 A:Status: translated from GR/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-159 <RES>
 A:Cross-references: EMBL:004507; NID:9545502; FIDN:AA050456.1; FID:9545503
 R:El-Deiry, W.S.; Tokino, T.; Waldman, T.; Velculescu, V.; Oliner, J.D.; Burrell, M.; Hill
 Cancer Res. 55, 2910-2919, 1995
 A:Title: Topological control of p21WAF1/Cip1 expression in normal and neoplastic tissues
 A:Reference number: 149296; MUID:95316868; PMID:7796420
 A:Accession: 149296
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GR/EMBL
 A:Molecule type: mRNA
 A:Residues: 1-159 <RES>
 A:Cross-references: EMBL:024173; NID:9902579; FIDN:AA052221.1; FID:9902579
 C:Genetics:

A:Gene: WAF1

Query Match 16.9%; Score 179.5; Db 2; Length 159;
 Best Local Similarity 26.4%; Pred. No. 2.4e-07;
 Matches 43; Conservative 18; Mismatches 65; Indels 53; Gaps 5;

QY 17 DAAQAEHPKPSACNLFPGVDHFEITPDLEKHCRCMDMEASQPKWNFDQNHKPIPGKYEW 76
 ||||| : : : : :
 Db 6 DVPVPVPH-RSKVCRCLFGPVDSEQLSRDCDALMAGCQAEARERWPDFVTEPLEGNFVW 64
 ||||| : : : : :
 QY 77 QEVEKGSILPEFYYP---PRPPKGACKVPAQESQDVSGSRPAAPLIGANSEDTHLVDP 133
 ||||| : : : : :
 Db 65 EPVPSLSLPRKVLSPGSPSLGSGIKPPSTSSALLQGPAP----- 105
 QY 134 KTDPSDSQTGLAFOCAGTAKKPAAPLIGANSEDTSTONKPNPTEENVSGSPNAGSVQIIPKKPQL 193
 ||||| : : : : :
 Db 106 -----EDHVALSLSLTIVSERP-----EDSPGGTSGTQ-----GR 135
 ||||| : : : : :
 QY 194 RRQQT 198
 ||||| : : : : :
 Db 136 RRQQT 140

RESULT 8
 A49438
 p53 tumor suppression mediator WAF1 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 07 Apr 1994 #sequence_revision 18 Nov 1994 #text_change 18 Nov 1994
 C:Accession: A49438
 R:El-Deiry, W.S.; Tokino, T.; Velculescu, V.E.; Levy, D.R.; Parsons, P.; Trent, J.M.;
 Cell 75, 817-825, 1993
 A:Title: WAF1, a potential mediator of p53 tumor suppression.
 A:Reference number: A49438, MUID:94061947, PMID:8242752
 A:Accession: A49438
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-143 <EIL>
 A:Note: sequence extracted from NCBI backbone (NCBIN:140807, NCBI:140808)

Query Match 16.6%; Score 176.5; Db 2; Length 143;
 Best Local Similarity 25.9%; Pred. No. 4e-07;
 Matches 48; Conservative 20; Mismatches 64; Indels 53; Gaps 5;

QY 17 DAAQAEHPKPSACNLFPGVDHFEITPDLEKHCRCMDMEASQPKWNFDQNHKPIPGKYEW 76
 ||||| : : : : :
 Db 6 DVPVPVPH-RSKVCRCLFGPVDSEQLSRDCDALMAGCQAEARERWPDFVTEPLEGNFVW 64
 ||||| : : : : :
 QY 77 QEVEKGSILPEFYYP---PRPPKGACKVPAQESQDVSGSRPAAPLIGANSEDTHLVDP 133
 ||||| : : : : :
 Db 65 EPVPSLSLPRKVLSPGSPSLGSGIKPPSTSSALLQGPAP----- 105
 QY 134 KTDPSDSQTGLAFOCAGTAKKPAAPLIGANSEDTSTONKPNPTEENVSGSPNAGSVQIIPKKPQL 193
 ||||| : : : : :
 Db 106 -----EDHVALSLSLTIVSERP-----EDSPGGTSGTQ-----GR 135
 ||||| : : : : :
 QY 194 RRQQT 198
 ||||| : : : : :
 Db 136 RRQQT 140

RESULT 9
 168674
 cyclin-dependent kinase - human (fragment)
 N:Alternate names: probable DNA synthesis inhibitor
 C:Species: Homo sapiens (man)
 C:Date: 04 Nov 1996 #sequence_revision 04 Nov 1996 #text_change 01 Dec 2000
 C:Accession: 168674; A34437; J53412; S39357
 R:Mousses, S.; Orzelik, H.; Lee, P.D.; Malkin, D.; Bull, S.B.; Andrulis, I.L.
 Hum. Mol. Genet. 4, 1089-1092, 1995
 A:Title: Two variants of the CIP1/WAF1 gene occur together and are associated with hu
 A:Reference number: 154380; MUID:95384154; PMID:7655464
 A:Accession: 168674
 A:Status: preliminary; translated from GB/EMBL/DDBJ

GenCore version 5.1.6
Copyright (c) 1993-2003 Compugen Ltd.

OM protein protein search, using sw model

Run on: May 30, 2003, 08:52:42, Search time: 44:56, Score: 1064
(without alignments)
972,808 Million cell updates/sec

Title: us-09-865-018b-2

Perfect score: 1064

Sequence: 1 MSNVRVSGSPSLERMDAPQ PNASGVPTPKKPKIPPRPT 198

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DR	ID	Description
1	1064	100.0	198	1	CDNB_HUMAN	P46527 homo sapien
2	994	93.4	198	1	CDNB_FELCA	O19001 felis silve
3	932	87.5	198	1	CDNB_CRICTUL	P06439 cricetulus
4	931	87.5	197	1	CDNB_MOUSE	P46414 mus musculus
5	870	81.8	178	1	CDNB_MUSVI	P46529 mustela vis
6	220.5	29.7	316	1	CDNC_HUMAN	P49918 homo sapien
7	212.5	20.0	448	1	CDNC_MOUSE	P49919 mus musculus
8	184.5	17.3	164	1	CDNL_FELCA	C13202 felis silve
9	179.5	16.9	159	1	CDNL_MOUSE	P39689 mus musculus
10	171.5	16.1	164	1	CDNL_HUMAN	P48436 homo sapien
11	98	9.2	1822	1	ZAP3_HUMAN	P40750 homo sapien
12	95	9.0	745	1	ADVA_PAT	Q64028 rattus norv
13	96	9.0	1278	1	Y232_HUMAN	Q65628 homo sapien
14	95	8.9	399	1	ALX4_MOUSE	O45137 mus musculus
15	94	8.8	735	1	ADDA_MOUSE	Q93YC0 mus musculus
16	93.5	8.8	556	1	HIF1_HUMAN	Q04711 homo sapien
17	91.5	8.6	1076	1	IF3A_CARTEL	P23388 caenorhabdi
18	89	8.4	611	1	IF4B_HUMAN	P23588 homo sapien
19	88.5	8.3	382	1	MYF_AVIIMB	P01104 avian myelo
20	88	8.3	446	1	CM3A_P15	P04404 sue scorla
21	88	8.3	1337	1	DEXT_STROO	P39653 streptococc
22	88	8.3	1461	1	TE1B_PRRVP	P11675 pseudorabie
23	87.5	8.2	559	1	ENL_HUMAN	Q03111 homo sapien
24	87.5	8.1	137	1	F327_APT1	Q0428 caenorhabdi
25	86	8.1	466	1	IMP2_PROME	P29681 drosophila
26	86	8.1	713	1	YU4_YEAS1	P39741 saccharomyc
27	86	8.1	1276	1	FRG3_HUMAN	Q38422 homo sapien
28	86	8.1	1495	1	CUTL1_MOUSE	P53564 mus musculus
29	85.5	8.0	514	1	WR44_ARATH	Q9X190 arabidopsis
30	85.5	8.0	525	1	MP11_PAT	P48465 rattus norv
31	85.5	8.0	2254	1	CCAG_PAT	Q54948 rattus norv
32	85	8.0	407	1	V338_HSV11	Q00115 tetralurid h
33	84.5	7.9	226	1	BASP_BOVIN	P80724 bos taurus

34	84.5	7.9	646	1	SGL_BOVIN	P23389 bos taurus
35	84	7.9	517	1	LADI_HUMAN	Q00515 homo sapien
36	84	7.9	531	1	SIS2_CANTP	Q12600 candida tro
37	84	7.9	574	1	SPKH_SYNY3	P74247 synchocyst
38	84	7.9	976	1	RPM2_ARATH	P92969 arabidopsis
39	84	7.9	1272	1	FMR2_MOUSE	Q55112 mus musculus
40	84	7.9	2842	1	APC_PAT	P70478 rattus norv
41	83.5	7.8	575	1	LNK_HUMAN	Q90432 homo sapien
42	83.5	7.8	811	1	BAS1_YEAST	P22035 saccharomyc
43	83.5	7.8	950	1	URB1_USTMA	P40349 ustilago ma
44	83.5	7.8	1181	1	HAIR_RAT	P97609 rattus norv
45	83.5	7.8	1203	1	YT41_CARCEL	Q11069 caenorhabdi

ALIGNMENTS

RESULT 1

ID	CDNB_HUMAN	STANDARD;	PRT;	198 AA.
AC	P46527; Q16307;			
DI	01-NOV-1995 (Rel. 32, Created)			
DI	01-NOV-1995 (Rel. 32, Last sequence update)			
DI	15-MAY-2002 (Rel. 41, Last annotation update)			
DE	Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase inhibitor p27) (p27Kip1).			
DE	Inhibitor p27 (p27Kip1).			
GN	CDKN1B OR Kip1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RF	SEQUENCE FROM N.A., AND SEQUENCE OF 28-79 AND 104-152.			
RC	TISSUE=Kidney;			
EX	MEDLINE=94306518; PubMed=8033212;			
PA	Polyak K., Lee M.-H., Erjument-Promage H., Koff A., Roberts J.M.,			
RA	Tempst P., Massague J.;			
RT	"Cloning of p27Kip1, a cyclin-dependent kinase inhibitor and a			
PT	potential mediator of extracellular antimitogenic signals."			
RL	Cell 78:59-66(1994).			
RN	[2]			
RF	SEQUENCE FROM N.A.			
EX	MEDLINE=45184144; PubMed=7882100;			
RA	Pietenpol J.A., Bohlender S.K., Sato Y., Papadopoulos N., Liu B.,			
PA	Friedman C., Trask B.J., Roberts J.M., Kinzler K.W., Rowley J.D.;			
RT	"Assignment of the human p27Kip1 gene to 12p13 and its analysis in			
RL	leukemias."			
RN	Cancer Res. 55:1206-1210(1995)			
RN	[3]			
RF	SEQUENCE FROM N.A., AND VARIANTS TPP-15 AND G1Y-109			
PA	Pfister M.T., Braun A.C., Montoya M.A., Chung M.-W., Nguyen C.P.,			
PA	Nguyen B.A., Livingston P.T., Paul G.L., Robertson P.D.,			
PA	Schackwitz W.S., Stenwood J.K., Wilk L.A., Nickerson P.A.,			
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RF	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 23-106 OF COMPLEX WITH CDK2			
EX	AND CG2A.			
EX	MEDLINE=96300319; PubMed=8684460;			
PA	Pusso A., Jeffrey P.D., Patton A.K., Massague J., Pavletich N.P.;			
PT	"Crystal structure of the p27Kip1 cyclin-dependent-kinase inhibitor			
RL	bound to the cyclin A-Cdk2 complex."			
RN	Nature 382:325-331(1996).			
CC	FUNCTION: Involved in G1 arrest. May mediate TGF-beta-induced G1			
CC	arrest. Inhibits complexes formed by cyclin D/CDK2,			
CC	cyclin A/CDK2, and cyclin D/CDK4. Interaction with nucleoprotein			
CC	NUP50 is required for nuclear import and for degradation of			
CC	phosphorylated p27Kip1 after nuclear import (By similarity)			
CC	FUNCTION: Interacts with NUP50 (By similarity).			
CC	SUBCELLULAR LOCATION: Nuclear.			
CC	TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES TESTED. HIGHEST			
CC	LEVELS IN SKELETAL MUSCLE, LOWEST IN LIVER AND KIDNEY.			
CC	DOMAIN: A PEPTIDE SEQUENCE CONTAINING ONLY AA 28-79 RETAINS			
CC	SUBSTANTIAL KIP1 CYCLIN A/CDK2 INHIBITORY ACTIVITY			

CC cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin
 CC NUP50 is required for nuclear import and for degradation of
 CC phosphorylated p27Kip1 after nuclear import (By similarity).
 CC -1- SUBUNIT: Interacts with NUP50 (by similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC FMRL: 049649; AAA25270.1; .
 CC InterPro: IPR003175; CDI.
 CC Pfam: PF02234; Cdi: 1.
 CC Cell cycle, Nuclear protein. NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 CC DOMAIN 153 169
 CC SEQUENCE 168 AA: 22349 MW: 28306 PAF55EAF6P9 CPO64;
 CC
 CC Query Match 87.6%; Score 932; DB 1; Length 198;
 CC Best Local Similarity 87.4%; Pred. No. 4.5e-62;
 CC Matches 173; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
 CC
 CC QY 1 MSNVVNSGSPSLERMDAPQAEHPKPSACPNIFGPDVHEEITPDLEKHCQPMEEASQKWK 60
 CC DB 1 MSNVVNSGSPSLERMDAPQAEHPKPSACPNIFGPDVHEEITPDLEKHCQPMEEASQKWK 60
 CC QY 61 NFDQNHKPLEGKYEWGEVEKSLPEFYYPFPKPKACVPAJESIVSSPKPAALIG 120
 CC DB 61 NFDQNHKPLEGKYEWGEVEKSLPEFYYPFPKPKACVPAJESIVSSPKPAALIG 120
 CC QY 121 APANSEDIHLVDPKILPSSSGLAFQWASLKKPAIDQSSDUNKKPAKTEENVSDGSPN 180
 CC DB 121 SCANSEDIHLVDPKILPSSSGLAFQWASLKKPAIDQSSDUNKKPAKTEENVSDGSPN 180
 CC QY 181 AGSVQTPKKPKGLRRK 196
 CC DB 181 AGSVQTPKKPKGLRRK 196
 CC
 CC RESULT 4
 CC CDB_MOUSE STANDARD; PPT. 197 AA
 CC AC P46414;
 CC DT 01-NOV-1995 (Rel. 32, Created)
 CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
 CC DT 15 JUN 2002 (Rel. 41, Last annotation update)
 CC DE Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase
 CC inhibitor p27) (p27Kip1).
 CC GN CDKN1B.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC OX NCBI_TaxID=10090;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC RX MEDLINE=94306519; PubMed=8033213;
 CC RA Toyoshima H., Hunter T.;
 CC RT "p27, a novel inhibitor of cyclin D3 protein kinase activity, is
 CC related to p21";
 CC RL Cell 78:67-74(1994).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC RX MEDLINE=94306518; PubMed=8033212;
 CC RA Poljak R., Lee M. H., Erdjument-Bromage H., Raff A., Roberts J.M.,
 CC RA Tempst P., Massague J.;
 CC RT "Cloning of p27Kip1, a cyclin-dependent kinase inhibitor and a
 CC potential mediator of extracellular antimitogenic signals";
 CC RL Cell 78:59-66(1994).

CC
 CC INTERACTION WITH NUP50, AND MUTAGENESIS.
 CC STRAIN-GALB/c;
 CC MEDLINE=2027197; PubMed=10811608;
 CC RA Mueller D., Thieme K., Ruegerlin A., Diekmann A., Eilers M.;
 CC RT "Cyclin E-mediated elimination of p27 requires its interaction with
 CC the nuclear pore-associated protein MNPAP60";
 CC PL EMBO J 19:3168-3180(2000).
 CC -1- FUNCTION: Involved in G1 arrest. May mediate TGF-beta-induced G1
 CC arrest. Binds to and inhibits complexes formed by cyclin E-CDK2,
 CC cyclin A-CDK2, and cyclin E1-CDK4. Interaction with nucleoporin
 CC NUP50 is required for nuclear import and for degradation of
 CC phosphorylated p27Kip1 after nuclear import.
 CC -1- SUBUNIT: Interacts with NUP50.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: U10440; AAA21149.1; .
 CC DB EMBL: U09968; AAA20235.1; .
 CC MGD: MGI:104565; Gdnkb.
 CC InterPro: IPR003175; Cdi.
 CC Pfam: PF02234; Cdi: 1.
 CC Cell cycle, Nuclear protein. NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 CC DOMAIN 153 169
 CC SEQUENCE 168 AA: 22349 MW: 28306 PAF55EAF6P9 CPO64;
 CC
 CC Query Match 87.5%; Score 931; DB 1; Length 197;
 CC Best Local Similarity 87.6%; Pred. No. 5.4e-62;
 CC Matches 172; Conservative 11; Mismatches 13; Indels 0; Gaps 0;
 CC
 CC QY 1 MSNVVNSGSPSLERMDAPQAEHPKPSACPNIFGPDVHEEITPDLEKHCQPMEEASQKWK 60
 CC DB 1 MSNVVNSGSPSLERMDAPQAEHPKPSACPNIFGPDVHEEITPDLEKHCQPMEEASQKWK 60
 CC QY 61 NFDQNHKPLEGKYEWGEVEKSLPEFYYPFPKPKACVPAJESIVSSPKPAALIG 120
 CC DB 61 NFDQNHKPLEGKYEWGEVEKSLPEFYYPFPKPKACVPAJESIVSSPKPAALIG 120
 CC QY 121 APANSEDIHLVDPKILPSSSGLAFQWASLKKPAIDQSSDUNKKPAKTEENVSDGSPN 180
 CC DB 121 SCANSEDIHLVDPKILPSSSGLAFQWASLKKPAIDQSSDUNKKPAKTEENVSDGSPN 180
 CC QY 181 AGSVQTPKKPKGLRRK 196
 CC DB 181 AGSVQTPKKPKGLRRK 196
 CC
 CC RESULT 5
 CC CDB_MOUSE STANDARD; PPT. 178 AA
 CC AC P46529;
 CC DT 01-NOV-1995 (Rel. 32, Created)
 CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
 CC DT 15 JUN 2002 (Rel. 41, Last annotation update)
 CC DE Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase
 CC inhibitor p27) (p27Kip1) (Fragment).
 CC GN CDKN1B.
 CC OS Mustela vison (American mink).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
 CC OC Mustela.
 CC OX NCBI_TaxID=9667;
 CC RN [1]
 CC SEQUENCE FROM N.A.

PX MEDLINE=94061997; PubMed=8242752;
 RA El-beiry W.S., Tokino T., Velculescu V.E., Levy D.B., Parsons R.,
 RA Trent J.M., Lin D., Mercer W.E., Kinzler K.W., Vogelstein B.;
 RT "WAF1, a potential mediator of p53 tumor suppression.";
 RL Cell 75:817-825(1993).
 RN [13]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94041955; PubMed=8254214;
 RA Xiong Y., Hannon G.T., Zhang H., Casso D., Kobayashi P., Beach D.;
 RT "p21 is a universal inhibitor of cyclin kinases.";
 RL Nature 366:701-704(1994)
 RN [14]
 RP SEQUENCE FROM N.A.
 RA Jiang H., Fisher P.B.;
 RT "Use of a sensitive and efficient subtractive hybridization protocol
 RT for the identification of genes differentially regulated during the
 RT induction of differentiation in human melanoma cells.";
 RL Mol Cell Differ 1:285-296(1993).
 RN [15]
 RP SEQUENCE FROM N.A.
 RA Jiang H., Lin J., Herlyn M., Kerbel R.S., Weissman B.E.,
 RA Welch D.R., Fisher P.B.;
 RT Submitted (May-1994) to the EMBL/GenBank/DBJ databases.
 RN [16]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94170884; PubMed=8125163;
 RA Noda A., Ning Y., Venable S.F., Pereira-Smith O.M., Smith T.P.;
 RT "Cloning of senescent cell-derived inhibitors of DNA synthesis using
 RT an expression screen.";
 RL Exp Cell Res 211:90-98(1994).
 RN [17]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95384154; PubMed=7655464;
 RA Mousses S., Gezelek H., Lee P.D., Malkin D., Bull S.B.,
 RA Andrulis I.L.;
 RT "Two variants of the CIP1/WAF1 gene occur together and are associated
 RT with human cancer.";
 RL Hum. Mol. Genet. 4:1089-1092(1995).
 RN [18]
 RP SEQUENCE FROM N.A. AND VARIANT ARG-31
 RA Pledier M.J., Braun A.C., Montoya M.A., Chung M.-W., Nguyen C.P.,
 RA Nguyen D.A., Livingston J.J., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Witlak L.A., Nickerson D.A.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases
 RN [19]
 RP SEQUENCE FROM N.A.
 RA Palmer S.;
 RL Submitted (Jul-1997) to the EMBL/GenBank/DBJ databases
 RN [10]
 RP SEQUENCE FROM N.A. AND VARIANT ARG-31.
 RC Tissue-Eye, and Lung;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 139-150.
 RX MEDLINE=97015085; PubMed=8861913;
 RA Gullis T.M., Felman Z., Hirsitz J., O'Donnell M., Kuriyan J.;
 RT "Structure of the C-terminal region of p1(WAF1/Cip1) complexed with
 RT human PCNA.";
 RL Cell 87:297-306(1996)
 CC -1- FUNCTION- MAY BE THE IMPORTANT INTERMEDIATE BY WHICH p53 MEDIATES
 CC ITS ROLE AS AN INHIBITOR OF CELLULAR PROLIFERATION IN RESPONSE TO
 CC DNA DAMAGE. MAY BIND TO AND INHIBIT CYCLIN-DEPENDENT KINASE
 CC ACTIVITY, PREVENTING PHOSPHORYLATION OF CRITICAL CYCLIN-DEPENDENT
 CC KINASE SUBSTRATES AND BLOCKING CELL CYCLE PROGRESSION.
 CC -1- SUBCELLULAR LOCATION- Nucleus
 CC -1- TISSUE SPECIFICITY- IS EXPRESSED IN ALL ADULT HUMAN TISSUES,
 CC WITH 5-FOLD LOWER LEVELS OBSERVED IN THE BRAIN.
 CC -1- INDUCTION- BY p53, MEZEPREIN (ANTIPIRENETIC COMPOUND) AND INTERFERON
 CC BETA.
 CC -1- SIMILARITY- THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR
 CC DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW= <http://www.infodivgen.fr/services/chrlocancer/genes/CIP1NIA10139.html>

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch)
 CC -----
 DE EMBL: L25610; AAA16109.1; -
 DE EMBL: S57388; AAB29246.1; -
 DE EMBL: U09579; AAA85641.1; -
 DE EMBL: U03106; AAC04313.1; -
 DE EMBL: L26165; AAA19811.1; -
 DE EMBL: L47233; AAB59560.1; ALT_INIT.
 DE EMBL: AF497872; AAM11787.1; -
 DE EMBL: Z45496; AAB06656.1; -
 DE EMBL: RC000275; AAH00275.1; -
 DE EMBL: BC001312; AAH00312.1; -
 DE EMBL: BC001935; AAH01935.1; -
 DE EMBL: BC013967; AAH13967.1; -
 DE PIR: S39357; S39357.
 DE SWISS-2DPAGE; P38936; HUMAN.
 DE GENE; HGNC:1784; CDKN1A.
 DE MIM; 116899; -
 DE InterPro; IPR003175; CDI.
 DE Pfam; PF02234; CDI; 1.
 KW Cell cycle; Nuclear protein; Zinc-finger; Polymorphism.
 FT ZN_FING 13 41
 FT DOMAIN 141 156
 FT VARIANT 31 31
 FT S->R (IN DBSNP:1801270).
 FT /FTID=VAP_011870.
 SQ SEQUENCE 164 AA; 18119 MW; 98D1E7C519ADFCA9 CRC64;
 Query Match 16.1%; Score 171.5; DR 1; Length 164;
 Best Local Similarity 31.4%; Pred. No. 2.8e-06;
 Matches 58; Conservative 20; Mismatches 58; Indels 49; Gaps 10;
 QY 17 DARGAHPKPS-ACRNLFGPVDHEELTRDLKHECRDMEEASQKWNFDONHKPLEGKYE 75
 DB 7 EVRQ--NPRVSKACRPLF;PVDSQLSPD'LALMAGCICQEARERNFDFVTETPLEGDA 64
 QY 76 WQVEKSLPEFYRPPKPGACKVFAQSVQVSSKFAAPLIGAFANSEUTHLVDPKT 135
 DB 65 WERVRLGLPKLYL-----PTG---PRRGDELUGGSR-----RPGT 97
 QY 136 LPSLSLGLAEAGAGIKKFAID--DSSTUNKVANKTEFNVSQSYNASVETPKKPL 193
 DB 98 SPALLQ-GTAE-----DHVDLSLSCILVPSGEG-AGGSPGGPLSQ-----GR 140
 QY 194 RRQT 198
 DB 141 KPGT 145
 RESULT 11
 ZAP3 HUMAN
 ZAP3 HUMAN STANCAFD; 18.00 AA.
 AC P49750; P49752; Q9P1V7;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Nuclear protein ZAP3 (ZAP113).
 GN ZAP3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pown T., Madan A., Olin S., Abbasi N., Baradarani L., Birditt B.,
 RA Bloom S., Dors M., Dinkhoff R., Fleetwood P., Harrison G., James R.,
 RA Kaur A., Madan A., Owen M.P., Ratcliffe A., Shaffer T., Hood L.;


```

QY 126 EPTH-----LVPRKTPSPDSQGLAFQACACIPKPRATPSUSSTONKPKANPRTERVNSG 177
Db 660 ERAHASPLLIQLPLADPPASASAGAPEVAS-----FATERGSPMDP-----SAG 707
QY 178 SPNAGSVFQTPKKPGIRPQ 197
Db 708 SFG---KSPKKKKK 719

RESULT 13
Y232_HUMAN          STANDARD          SPT: 1278 AA.
AC GQ2628:
DT 01-NOV-1997 (Rel. 45, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein KIA0232 (Fragment).
GN KIA0232.
OS Homo sapiens (Human).
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
OC Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
OC NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN 12
RP SEQUENCE OF 271-1278 FROM N.A.
RA TISSUE=Rone marrow;
RX MPM1NF=07101544; PubMed=9039502;
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.
RT "Prediction of the coding sequences of unidentified human genes VI.
RT The coding sequences of 80 new genes (KIA0201-KIA0280) deduced by
RT analysis of cDNA clones from cell line KG-1 and brain #;
RL DNA Res. 3:321-329(1996).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D86985; AAA13221.2; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 1278 AA; 141663 MW; 24070847/APR1440 CPM4;
-----
Query Match          9.0%, Score 96, OR 1, Length 1278;
Best Local Similarity 26.7%, Pred. No. 9, 3;
Matches 47; Conservative 21; Mismatches 62; Indels 46; Gaps 11;
QY 39 PELTRFKPKTMEASAKWVFPQNIKFLFY-----KYRWLEVERKSLFEFFYE EF 92
Db 11 ETIVPELCKLGLGKSKQEK-----LHKLENSPSPEAELSPPAKQV-EMVVEAFPP 64
QY 93 KFKKAE-----KVPALSSQVSSSPFAHLIFATANSFHLIVKTKTPSSLSQ 141
Db 64 LSKFPVTLGEMIVNKRKSKVSYSSSSSSSTAPPA-----SLTSS--SPKDNSESE 114
QY 142 TSLAECACIPKPPATPSSTSKPKANPRTERVNSVSTNAGSVETPKKKPKIRPQ 197
Db 114 V-TKRSSEV---PTTVHKTSKSKNKENFSN-----GTIER---KPAIYKKQ 157

PEPSET 14
ALX4_MOUSE
ID ALX4_MOUSE          SPT: 399 AA
AC Q35137;

```

```

DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein aristaless-like 4 (ALX-4).
GN ALX4.
OS Mus musculus (Mouse).
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
OC Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
OC NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6; TISSUE=Embryo;
RX MEDLINE=9808522; PubMed=9426253;
RA Qu S., Li J., Wisdom P.;
RT "Alx-4: cDNA cloning and characterization of a novel paired-type
RT homeodomain protein.";
RL Gene 203:217-233(1997).
RN 12
RP VARIANT LST GLN-206.
RX MEDLINE=98301426; PubMed=9636085;
RA Co S., Tucker S.C., Ehrlich J.S., LeVorse T.M., Flaherty L.A.,
RA Wisdom R., Vogt T.F.;
RT "Mutations in mouse Aristaless-like4 cause Strong's luxoid
RT polydactyly.";
RL Development 125:2711-2721(1998).
CC 1- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN SKULL AND LIMB
CC DEVELOPMENT.
CC 1- SUBUNIT: BINDS DNA.
CC 1- SUBCELLULAR LOCATION: Nuclear.
CC 1- TISSUE SPECIFICITY: EXPRESSED IN OSTEOBLASTS, NOT EXPRESSED IN
CC BRAIN, HEART, INTESTINE, KIDNEY, LIVER, MUSCLE, SPLEEN AND TESTIS.
CC 1- DEVELOPMENTAL STAGE: EXPRESSED FROM E8.25 AND CONFINED TO
CC MESENCHYMAL CELLS THROUGHOUT THE EMBRYO DEVELOPMENT. EXPRESSION IS
CC SEEN AT SEVERAL SITES, INCLUDING CRANIOFACIAL REGION, FIRST
CC BRANCHIAL ARCH AND ANTERIOR ASPECT OF THE LIMB BUD.
CC 1- DISEASE: DEFECTS IN ALX4 AFFECT THE CAUSE OF STRONG'S LUXOID (LST)
CC PHENOTYPE. AT HETEROZYGOSITY LST IS CHARACTERIZED BY PREAXIAL
CC ABNORMALITIES OF THE HINDFEET AND, VERY RARELY, OF THE FOREFEET.
CC HOMOLOGUES SHOW PREAXIAL POLYDACTYLY OF ALL FOUR LIMBS.
CC REDUCTIONS AND DUPLICATIONS OF THE PADIUS, ABSENCE OF THE TIBIA,
CC CRANIOFACIAL DEFECTS, REDUCTION OF THE PHRIS, AND DORSAL ALOPECIA.
CC 1- SIMILARITY: BELONGS TO THE PAIRED HOMEBOX FAMILY.
CC 1- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.
CC 1- SIMILARITY: CONTAINS 1 OAP DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF051455; AAC39943.1; -.
RX HSSEF; PUB601; IFFL.
RX MGI: MGI:108359; ALX4.
DR InterPro: IPR003654; Homeo_OAP.
DR InterPro: IPR001456; Homeobox
DR Pfam: PF00046; homeobox; 1.
DR ProDom: PD00010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS50071; HOMEBOX_2; 1.
DR PROSITE: PS5803; OAP; 1.
KW Homeobox DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation; Activator; Disease mutation.
FT DNA_BIND 202..261 HOMEBOX.
FT DOMAIN 379..392 OAR.
FT VARIANT 206..206
FT SEQUENCE 399 AA; 42762 MW; 2401920NCA31D25 CPM64;

```


Genore version 5.1.6
Copyright (c) 1993-2003 Computer i.i.d.

OM protein - protein search, using sw mode!

Run on: May 30, 2003, 08:53:57 ; Search time 34.5449 seconds
(without alignments)
1181.337 Million cell updates/sec

Title: US-09-865-018b-2
Perfect score: 1064
Sequence: 1 MSNVRVNSGSPSEFMARQ

Scoring table: R09NM62 PNAQSVPLPKKELKPKKEL 198

Gapop 10 0 , Gapext 0 5

Searches: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2060000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_minc:*
- 8: sp_orcellule:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_ricent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvtrus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1058	99.4	198	4	Q9NYG6	Q9nyg6 homo sapien
2	1057	99.3	198	4	Q9N8U6	Q9n8u6 homo sapien
3	1054	99.1	198	4	Q96TE0	Q96te0 homo sapien
4	976	91.7	198	6	Q9BDC3	Q9bdc3 sus scrofa
5	924	86.8	197	11	Q08769	Q08769 rattus norv
6	619	86.4	197	11	Q35792	Q35792 rattus norv
7	852	80.1	158	4	Q43806	Q43806 homo sapien
8	762	71.6	172	6	Q9BEA5	Q9bea5 sus scrofa
9	347	32.6	179	13	Q90VX4	Q90vx4 brachydanio
10	218	20.5	210	13	Q91663	Q91663 xenopus lae
11	214	20.1	42	4	Q90H60	Q90h60 homo sapien
12	214	20.1	259	13	Q91646	Q91646 xenopus lae
13	211	19.8	335	11	Q91V06	Q91v06 mus musculu
14	191	18.0	164	11	Q64315	Q64315 rattus norv
15	190	17.9	42	11	Q9QX80	Q9qx80 rattus norv
16	172	15.2	164	4	Q964F1	Q964f1 homo sapien

17	170.5	16.0	181	4	Q14010	Q14010 homo sapien
18	151.5	14.2	258	5	Q22198	Q22198 caenorhabdi
19	141	13.3	259	5	Q908K5	Q908k5 caenorhabdi
20	125	11.7	184	5	Q22197	Q22197 caenorhabdi
21	110.5	10.4	253	5	Q8WQ22	Q8wq22 drosophila
22	102	9.6	518	5	Q960X2	Q960x2 drosophila
23	102	9.6	1465	5	Q9WMD0	Q9wmd0 drosophila
24	102	9.6	1645	5	Q8WSS9	Q8wss9 drosophila
25	100	9.4	191	10	Q04154	Q04154 arabidopsis
26	100	9.4	191	10	Q828U9	Q828u9 arabidopsis
27	100	9.4	341	10	Q888Q3	Q888q3 arabidopsis
28	98.5	9.3	245	5	Q94536	Q94536 drosophila
29	98.5	9.3	755	4	Q43714	Q43714 homo sapien
30	98.5	9.3	883	4	Q94MNR	Q94mnr homo sapien
31	98	9.2	795	5	Q950G2	Q950g2 toxoplasma
32	97	9.1	255	5	Q91654	Q91654 drosophila
33	96.5	9.1	245	5	Q91658	Q91658 drosophila
34	95	8.9	393	10	Q858M4	Q858m4 arabidopsis
35	95	8.9	1173	11	Q62018	Q62018 mus musculu
36	94.5	8.9	1008	10	Q9FNE4	Q9fne4 arabidopsis
37	94	8.8	246	3	Q03973	Q03973 saccharomyc
38	94	8.8	637	11	Q8R149	Q8r149 mus musculu
39	94	8.8	861	5	Q21186	Q21186 caenorhabdi
40	94	8.8	364	4	Q9Y554	Q9y554 homo sapien
41	94	8.8	3664	4	Q96T58	Q96t58 homo sapien
42	93.5	8.8	500	11	Q922K1	Q922k1 mus musculu
43	93.5	8.8	798	10	Q94DW7	Q94dw7 oryza sativ
44	93.5	8.8	1307	11	Q88974	Q88974 mus musculu
45	93.5	8.8	1323	4	Q90K50	Q90ke0 homo sapien

ALIGNMENTS

RESULT 1

Q9NYG6 PRELIMINARY: PRT: 198 AA.

AC Q9NYG6; DT 01-OCT-2000 (Tremblrel. 15, Created)
 DI 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Cyclin-dependent kinase inhibitor p27kip1.
 OS Homo sapiens (Human).
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
 OC Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 OX NCRL_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 KC TISSUE=HEPATOMA;
 RA Li J, Wang W-L, Yang X-K, Yu X-X ;
 PT "Homo sapiens cyclin dependent kinase inhibitor p27kip1 cDNA";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF247551; AAF69497.1;
 DR InterPro: IPR003175; CDI;
 DR Pfam: PF02234; CDI; 1.
 KW Kinase.

Q9 NYG6 SEQUENCE 198 AA: 22099 MW: 407D589UICDF4EA CRC64;

Query Match 99.4%; Score 1058; DB 4; Length 198;
 Best local Similarity 99.5%; Pred No 6,5e-82;
 Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy	1	MSNVRVNSGSPSEFMARQAEHPKPSATPNLEGPVDHBEELTPDLKHPDMEFASQRKW	60
Db	1	MSNVRVNSGSPSEFMARQAEHPKPSATPNLEGPVDHBEELTPDLKHPDMEFASQRKW	60
Cy	61	NFQFQNHKFLGKYEWEVERKSSLPFFYFPPPPKAGAKVPAFESSVSSPPAPFLIG	120
Db	61	NFQFQNHKFLGKYEWEVERKSSLPFFYFPPPPKAGAKVPAFESSVSSPPAPFLIG	120
Cy	121	APANSFTHLVKPKTPSPSSQDGLAPFAGAPKPPPAIHSSTONKFPANPTEENVSPSPN	180
Db	121	APANSFTHLVKPKTPSPSSQDGLAPFAGAPKPPPAIHSSTONKFPANPTEENVSPSPN	180


```

DE Cyclin dependent kinase inhibitor p27 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX [1]
RP SEQUENCE FROM N.A.
RA Waltrney D., Loda M.;
RT "Homo sapiens cyclin-dependent kinase inhibitor p27 intron.";
PL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF213700; AAF21068.1; -
KW Kinase.
FT NON_TER 1
FT NON_TER 42
FT NON_TER 42
SQ SEQUENCE 42 AA: 4461 MW, 92837498.2A590CD9 CRCK64;

Query Match 20.1%, Score 214; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.1e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 LAFCAGAGPKPPATPDSSQNKPRNPTFFNVSDGSPNAGSVE 185
DB 1 LAEQACAGTAKKPPATPDSSQNKPRNPTFFNVSDGSPNAGSVE 42

RESULT 12
Q91646 PRELIMINARY; PRT; 209 AA
AC Q91646;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-DEC-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cyclin-dependent kinase inhibitor p28.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
OC Amphibia; Batrachia, Anura, Mesokotrichia, Pipiloidea; Pipilidae;
OC Xenopodinae; Xenopus.
ON NCBI_TaxID=8355;
RX [1]
RP SEQUENCE FROM N.A.
RA Shou W., Dunphy W.G.;
RT Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases
DR EMBL: U38844; AAC59775.1; -
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1.
KW Kinase.
SQ SEQUENCE 209 AA: 23475 MW, AP9AVALA247400; CRCK4,

Query Match 20.1%, Score 214; DB 13; Length 209;
Best Local Similarity 27.9%; Pred. No. 1.4e-10;
Matches 56; Conservative 38; Mismatches 79; Indels 28; Gaps 6;

QY 14 BRMDARQEHKPS-----ACRNLFQFVDHEELTRDLKLEKRCMDMEASQKKNWFQNH 67
DB 10 FEMISAPAVILFRLNGTGGAAKRLNPAPLHDEMPSLKKGLKELQASDQPPNWFQPEIS 69
QY 68 KPIFGKYPQWKEVSGSLPEFYPPFPFKGACKVPAGESQVSGSRPAAPLIGAPANSEJ 127
DB 70 TPLKJFCQWEPVESKOMPSEYSONPSTAAANTPSPKQV-QELLVSPKPEPEAPVITV 128
QY 128 THLVDFKTFSSQTGLAQAGAKKFAIGSSQNKRRNK-----IEENVSD 176
DB 129 NVNPNPCAKNAEKL--VNRQGVK-GRKASANTSTQRRKREITPILDYFKKKKILS 185
QY 177 GSPNAGS-----VEQTPKK 190

```

```

DB 186 AKPLATKGAHLTCLPLEUTPRK 206

RESULT 13
Q91V06 PRELIMINARY; PPT; 335 AA
AC Q91V06;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cyclin dependent kinase inhibitor 1C (p57Kip2 protein) (P57).
GN CDKN1C OR P57KIP2.
OS Mus musculus domesticus (western European house mouse), and
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae; Murinae; Mus.
ON NCBI_TaxID 10092; 10090;
RX [1]
RP SEQUENCE FROM N.A.
RA Engemann S., Stroeder M., Paulsen M., Franck O., Reinhardt R.,
RA Lane N., Reik W., Walter J.;
RT "Sequence and functional comparison in the Beckwith-Wiedemann region:
RT implications for a novel imprinting centre and extended imprinting.";
PL Hum Mol Genet 9:2691-2706(2000)
RN [2]
RP SEQUENCE FROM N.A.
RA Engemann S.;
RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RX [3]
RP SEQUENCE FROM N.A.
RA John P.M., Hodges M., Little P., Barton S., Surani M.A.;
RT "A human p57KIP2 transgene is not activated by passage through the
RT maternal mouse germline.";
PL Hum Mol Genet 8:2211-2219(1999)
RN [4]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases
DR EMBL: AJ276505; AAC16402.1; -
DR EMBL: AF160190; AAF00983.1; -
DR EMBL: BC005412; AAH05412.1; -
DR MGI: 104564; Cdkn1c
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1.
KW Kinase.
SQ SEQUENCE 335 AA: 35903 MW, E5C40675287FEB3F CRCK64;

Query Match 19.8%, Score 211; DB 11; Length 335;
Best Local Similarity 30.9%; Pred. No. 4.5e-10;
Matches 65; Conservative 38; Mismatches 60; Indels 46; Gaps 8;

QY 25 KPSACRNLFQFVDHEELTRDLKLEKRCMDMEASQKKNWFQNHKPLE--GKVEWQEVK 82
DB 15 RSSACRSLFQFVDHEELTRDLKLEKRCMDMEASQKKNWFQNHKPLE--GKVEWQEVK 74
QY 83 SLPEFYPP-----PPPKACKV-----PAGESQVSGSRPAAPLIGAPANS 125
DB 75 SVIAPFYPPVQVSGVRLQGLQPPPPVAVAVIIPSSCHPAGKAPGKLEAPKQPPSAPASA 133
QY 126 EFTHLVFPKTPFSQGLAEVAGTIPKPPATPDSS-----TPNKKANKPIENVSDGSP 179
DB 134 -----VVAETPPA-----TPAPASLTSDPITPEVTLVAISDFIPDIPDAMP 176
QY 180 NAGS-----VEQTPKK 190
DB 177 DVATRDGEEQVPEQ 190

```


GenCore version 5.1.5
Copyright (c) 1994 - 2004, Compugen Ltd

OM protein - protein search, using sw model

Run on: May 30, 2003, 08:52:12 : Search time 14.7158 Seconds
(without alignments)
606.682 Million cell updates/sec

Title: US-09-865-018b-2_AAY_22_88

Perfect score: 383

Sequence: 1 FHPKPSACPNLPGVDHREI..... PLEKYVQVPRKSLPEFY 67

Scoring table: BLOSUM62

Gap: 10.0, Gap-ext: 0.5

Searched: 908470 seqs 13250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 240000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A:Geneseq_101002.*
1: /SID2/qcdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID2/qcdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID2/qcdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID2/qcdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SID2/qcdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SID2/qcdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SID2/qcdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SID2/qcdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SID2/qcdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SID2/qcdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SID2/qcdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SID2/qcdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SID2/qcdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID2/qcdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SID2/qcdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SID2/qcdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SID2/qcdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SID2/qcdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SID2/qcdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID2/qcdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID2/qcdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID2/qcdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID2/qcdata/geneseq/geneseq-emb1/AA2002.DAT.*

pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	383	100.0	167	20	AAW95101
2	383	100.0	177	21	AAW97530
3	383	100.0	177	21	AAW96045
4	383	100.0	177	21	AAW96072
5	383	100.0	194	20	AAW94940
6	383	100.0	144	16	AAW97914
7	383	100.0	198	17	AAW92709
8	383	100.0	198	19	AAW9717
9	383	100.0	194	19	AAW46988
10	383	100.0	198	20	AAW00768

11	383	100.0	198	21	AAW97523	Human p27 protein
12	383	100.0	198	21	AAW96052	Human cyclin depen
13	383	100.0	198	21	AAW96066	Human cyclin depen
14	383	100.0	198	21	AAW70307	Human mutant cycli
15	383	100.0	198	21	AAW44400	Human p27(Kip1) ki
16	383	100.0	198	22	AAW84649	Amino acid sequenc
17	383	100.0	198	22	AAW48309	Human p27 protein.
18	383	100.0	198	23	AAW47880	Human p27 protein.
19	383	100.0	334	20	AAW95103	Truncated p27/p16
20	383	100.0	334	21	AAW97532	Human W8 protein s
21	383	100.0	334	21	AAW96047	Antiproliferative
22	383	100.0	334	21	AAW96074	Angiogenesis inh
23	383	100.0	348	20	AAW95104	Truncated p27/p16
24	383	100.0	348	21	AAW97531	Human W7 protein s
25	383	100.0	348	21	AAW96046	Antiproliferative
26	383	100.0	348	21	AAW96073	Angiogenesis inh
27	383	100.0	365	18	AAW23536	CDK inhibitory fus
28	383	100.0	365	20	AAW95107	Human p16p27 fusio
29	383	100.0	365	20	AAW95096	Human p16p27 fusio
30	383	100.0	365	21	AAW97527	Human W4 protein s
31	383	100.0	365	21	AAW97529	Human W6 protein s
32	383	100.0	365	21	AAW96042	Antiproliferative
33	383	100.0	365	21	AAW96044	Antiproliferative
34	383	100.0	365	21	AAW96069	Angiogenesis inh
35	383	100.0	365	21	AAW96071	Angiogenesis inh
36	383	100.0	380	18	AAW23535	CDK inhibitory fus
37	383	100.0	380	20	AAW45095	Human p16(GSp27 f
38	383	100.0	380	21	AAW97528	Human W5 protein s
39	383	100.0	380	21	AAW96043	Antiproliferative
40	383	100.0	380	21	AAW96070	Angiogenesis inh
41	383	100.0	391	18	AAW23534	CDK inhibitory fus
42	383	100.0	391	20	AAW95094	Human p27-p16 tusi
43	383	100.0	391	21	AAW97526	Human W3 protein s
44	383	100.0	391	21	AAW96041	Antiproliferative
45	383	100.0	391	21	AAW96068	Angiogenesis inh

ALIGNMENTS

RESULT 1

AAW95101 standard. Protein: 167 AA.

XX AAW95101:

XX AC

XX 25-MAY-1999 (first entry)

XX DT

XX DB

XX XX

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

P1 Novel recombinant lentivirus for inhibiting proliferation of smooth
 PT muscle cells in e.g. restenosis, is replication deficient and comprises
 XX a transgene encoding a cyclin dependent kinase inhibitor

PS Example 1, Page 109-110, 126pp, English.

XX The present sequence is that of truncated human p27 protein in
 CC which the first 12 N-terminal and the final 21 C-terminal amino
 CC acids of full-length p27 (see AAY96052) are deleted to remove a CDK
 CC consensus phosphorylation site at amino acids 187-190, a potential
 CC phosphorylation site for proline-directed kinases at amino acids
 CC 178-181 and a weak CDK phosphorylation site at amino acids 10-13.
 CC p27 is a cyclin dependent kinase inhibitor (CKI). A claimed
 CC method for inhibiting smooth muscle cell hyperproliferation involves
 CC transducing smooth muscle cells with a replication-deficient
 CC recombinant adenovirus that lacks a functional E1 region and a
 CC functional E4 region, and comprises a transgene encoding a CKI.
 CC The CKI is an INK4 family protein such as human p16, a CIP/KIP
 CC family protein such as p27, active fragments of these, e.g.
 CC p27(12-178aa), or fusion proteins comprising (active fragments of)
 CC an INK4 family protein and a CIP/KIP family protein (see AAY96046 and
 CC AAY96049). The method is used to inhibit mammalian smooth muscle
 CC cell hyperproliferation induced by injury caused by angioplasty,
 CC stent placement or vein engraftment. It is useful for treating
 CC vascular pathologies, e.g. restenosis. Also claimed are recombinant
 CC lentiviruses encoding CKIs. Use of truncated p27 was designed to
 CC increase the protein's half-life and to eliminate potential
 CC phosphorylation sites involved in the negative regulation of CKI
 CC activity.

XX Sequence 177 AA:

Query Match. 100.0%; Score 383; DB 21; Length 177;
 Best Local Similarity 100.0%; Pied. NO. 8.2e-41;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHKPSACRNLPGVVDEELIKMFKHCIMPFASQPKKNFQPNHKPLPGKYWEVEK 50
 DB 22 EHKPSACRNLPGVVDEELIKMFKHCIMPFASQPKKNFQPNHKPLPGKYWEVEK 81

QY 61 GSLPEFY 67

DB 82 GSLPEFY 88

RESULT 4

ID AAY96072 standard; Protein: 177 AA.

AC AAY96072;

XX 05-DEC-2000 (first entry)

XX Human cyclin dependent kinase inhibitor p27(12-178).

XX Cyclin dependent kinase inhibitor, CKI, CIP, KIP, human, p27,

XX angiogenesis, inhibitor, neoplasia; rheumatoid arthritis;

XX endometriosis; psoriasis; vascular retinopathy; cytostatic;

XX antirheumatic; antineoplastic; gynaecological; antipsoriatic;

XX antiproliferative; gene therapy; mutant; mutagen.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FI Peptide 1..11

FI Protein /label= Haemagglutinin-epitope

FI Protein 12..177

XX Key Location/Qualifiers

PN W0200002159-A1.

XX 08-SEP-2000.

XX 28-FEB-2000; 2000W0-0504970.

XX 01-MAP-1999; 00NS-0122974.

XX 06-NOV-1999; 00NS-0163682.

XX 09-DEC-1999; 99US-0457646.

XX (CELL-) CELL GENESYS INC.

XX (MITO-) MITOTIX INC.

XX Patel S, McArthur J, Gyuris J;

XX WPT: 2000-565501/52.

XX N-PSDB; AAA50527.

XX Inhibiting angiogenesis and treating angiogenesis-associated
 PT conditions, e.g. neoplasia, psoriasis by transducing an endothelial
 PT cell with a recombinant virus having a transgene encoding a cyclin
 PT dependent kinase inhibitor

PS Example 1; Page 117-118; 138pp; English.

XX The present sequence is that of a truncated human p27 protein in
 CC which the first 12 N-terminal and the final 21 C-terminal amino
 CC acids of full-length p27 (see AAY96066) are deleted to remove a CDK
 CC consensus phosphorylation site at amino acids 187-190, a potential
 CC phosphorylation site for proline-directed kinases at amino acids
 CC 178-181 and a weak CDK phosphorylation site at amino acids 10-13.
 CC p27 is a cyclin dependent kinase inhibitor (CKI) that inhibits
 CC angiogenesis. A claimed method for inhibiting angiogenesis
 CC involves transducing an epithelial cell with a transgene encoding
 CC (internalizable, secretable) CKI. The delivery system for the
 CC transgene may be a liposome or a recombinant virus. The CKI is
 CC a protein of the CIP/KIP family such as p27, a protein of the
 CC INK4 family such as p16, active fragments of these proteins (e.g.
 CC amino acids 25-93 or 12-178 of human p27), or a fusion protein
 CC comprising 2 CKI proteins such as (truncated) p27 and p16 (see
 CC AAY96068-80). The method is used to treat conditions associated with
 CC angiogenesis, e.g. neoplasia, rheumatoid arthritis, endometriosis,
 CC psoriasis and vascular retinopathy (claimed). Alternatively, the
 CC transgene is delivered to an auxiliary cell, and is expressed by
 CC that cell such that the CKI is released into the blood and
 CC contacts the target epithelial cell. Use of truncated p27 was
 CC designed to increase the protein's half-life and to eliminate
 CC potential phosphorylation sites involved in the negative
 CC regulation of CKI activity.

XX Sequence 177 AA;

Query Match 100.0%; Score 383; DB 21; Length 177;

Best Local Similarity 100.0%; Pied. NO. 8.2e-41;

Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 EHKPSACRNLPGVVDEELIKMFKHCIMPFASQPKKNFQPNHKPLPGKYWEVEK 60

DB 22 EHKPSACRNLPGVVDEELIKMFKHCIMPFASQPKKNFQPNHKPLPGKYWEVEK 81

QY 61 GSLPEFY 67

DB 82 GSLPEFY 88

RESULT 5

AAW94930

ID AAW94930 standard; Protein: 194 AA.

XX AAW94930;

XX 11-MAY-1999 (first entry)

XX Amino acid sequence of p27 protein.

XX Vascular proliferative disease, p27 protein; fusion protein; restenosis;

KW p27 protein; Kipl; cyclin E; Cdk2; cell proliferation; ulcer;
 KW cancer; hyperplasia; diagnosis; therapy.

XX Homo sapiens.

XX W09602140-A1.

XX 01-FEB-1996.

XX 07-JUN-1995; 95WO-US07361

XX 15-MAY-1994; 94US-0275483

XX (HUTCHINSON CANCER RES CENT FRED.

XX (SLAK) SUGAN KETTERING INST CANCER RES.

XX Koff A, Massague J, Polyak K, Roberts JM;

XX WPI; 1996-105554/11.

XX N-PSDB; AAL16436.

XX p27 is an inhibitor of cyclin E-Cdk2 complex activation and agents
 PT which enhance and inhibit its activity; useful for treating
 PT hyperproliferative and hyperproliferative disorders.

XX Disclosure; Fig 15a-b; 129pp; English.

XX A cDNA clone (AAL16336) derived from human kidney codes for a 27
 CC kDa protein, p27 Kipl (AAR92709), that is capable of binding to
 CC and inhibiting the activation of a cyclin E-Cdk2 complex. Human
 CC Kipl shows a high degree of homology to mink (AAR92707) and mouse
 CC (AAR92708) Kipl proteins, and the N terminal half of the protein shows
 CC significant homology to Cip1/WAF1. Kipl shows cdk inhibitory
 CC activity and prevents cdk2 activation. Overexpression inhibits
 CC cell entry to the S phase. Kipl can be produced by expression of
 CC the cDNA clone in cultured cells. It can be used in vitro
 CC assays to screen agents that affect p27 activity, and in methods
 CC for the diagnosis and treatment of hyperproliferative disorders,
 CC e.g. ulcer, and hyperproliferative disorders, e.g. cancer and
 CC hyperplasia.

XX Sequence 198 AA:

Query Match 100.0%; Score 383; DB 17; Length 198;
 Best Local Similarity 100.0%; Pred No. 9.4e-41;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 EHKPSACNIFGPGVDFHEELTPILEKHCPTMEERASQPKWNFDQNHKPLEGKYWQVEVK 60
 |||||
 DB 22 EHKPSACNIFGPGVDFHEELTPILEKHCPTMEERASQPKWNFDQNHKPLEGKYWQVEVK 61

QY 61 GSLPEFY 67

DB 82 GSLPEFY 88

RESULT 8

AAW29717

ID AAW29717 standard; Protein: 198 AA.

XX AAW29717;

XX 27-OCT-1998 (first entry)

DE 27 kDa protein inhibiting activation of cyclin E-Cdk2 complex.

XX 27 kDa protein; p27; Kipl; inhibits activation; cancer; breast carcinoma;
 KW cyclin E-cyclin dependent kinase complex; hyperproliferative disease;
 KW recurrence; treatment; human.

XX Homo sapiens.

XX W09834121-A2.

XX 06-AUG-1998.
 XX 04-FEB-1998; 98WO-US01893.
 XX 03-FEB-1997; 97US-0794002.
 XX (HUTCHINSON CANCER RES CENT FRED.

XX Porter PL, Roberts JM;

XX WPI; 1996-447612/37.

XX N-PSDB; AAV47517.

XX Assays for protein p27 inhibiting activation of cyclin E-cdk2
 PT complex - useful for, e.g. diagnosis and prognosis of cancer,
 PT especially breast carcinoma

XX Claim 18, Fig 15B; 105pp; English.

XX The present sequence represents a 27 kDa protein (p27 or Kipl) which
 CC inhibits the activation of a cyclin E-cyclin dependent kinase (cdk2)
 CC complex. A reduced relative level of Kipl is indicative of a
 CC hyperproliferative disease (particularly cancer, especially breast
 CC carcinoma) and also is prognostic for increased risk of death and/or
 CC recurrence of cancer (and may be used to determine suitable treatments).
 CC Agents that affect the activity of Kipl can be used to treat
 CC hyperproliferative conditions, e.g. to stimulate tissue or organ repair
 CC or to establish cell cultures.

XX Sequence 198 AA:

Query Match 100.0%; Score 383; DB 19; Length 198;
 Best Local Similarity 100.0%; Pred No. 9.4e-41;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHKPSACNIFGPGVDFHEELTPILEKHCPTMEERASQPKWNFDQNHKPLEGKYWQVEVK 60
 |||||
 DB 22 EHKPSACNIFGPGVDFHEELTPILEKHCPTMEERASQPKWNFDQNHKPLEGKYWQVEVK 81

QY 61 GSLPEFY 67

DB 82 GSLPEFY 88

RESULT 9

AAW46888

ID AAW46888 standard; Protein: 198 AA.

XX AAW46888;

XX 15-JUN-1998 (first entry)

DE Amino acid sequence of the p27Kipl protein.

XX E7 oncoprotein; proliferative state; HPV; kinase activity;
 KW cyclin/cyclin-dependent kinase; p21Cip1; interaction; inactivation;
 KW cyclin/cyclin-dependent kinase inhibitor.

XX Homo sapiens.

XX US5736318-A.

XX 07-APR-1998.

XX 17-MAR-1995; 95US-0406248.

XX 17-MAY-1995; 95US-0406248.

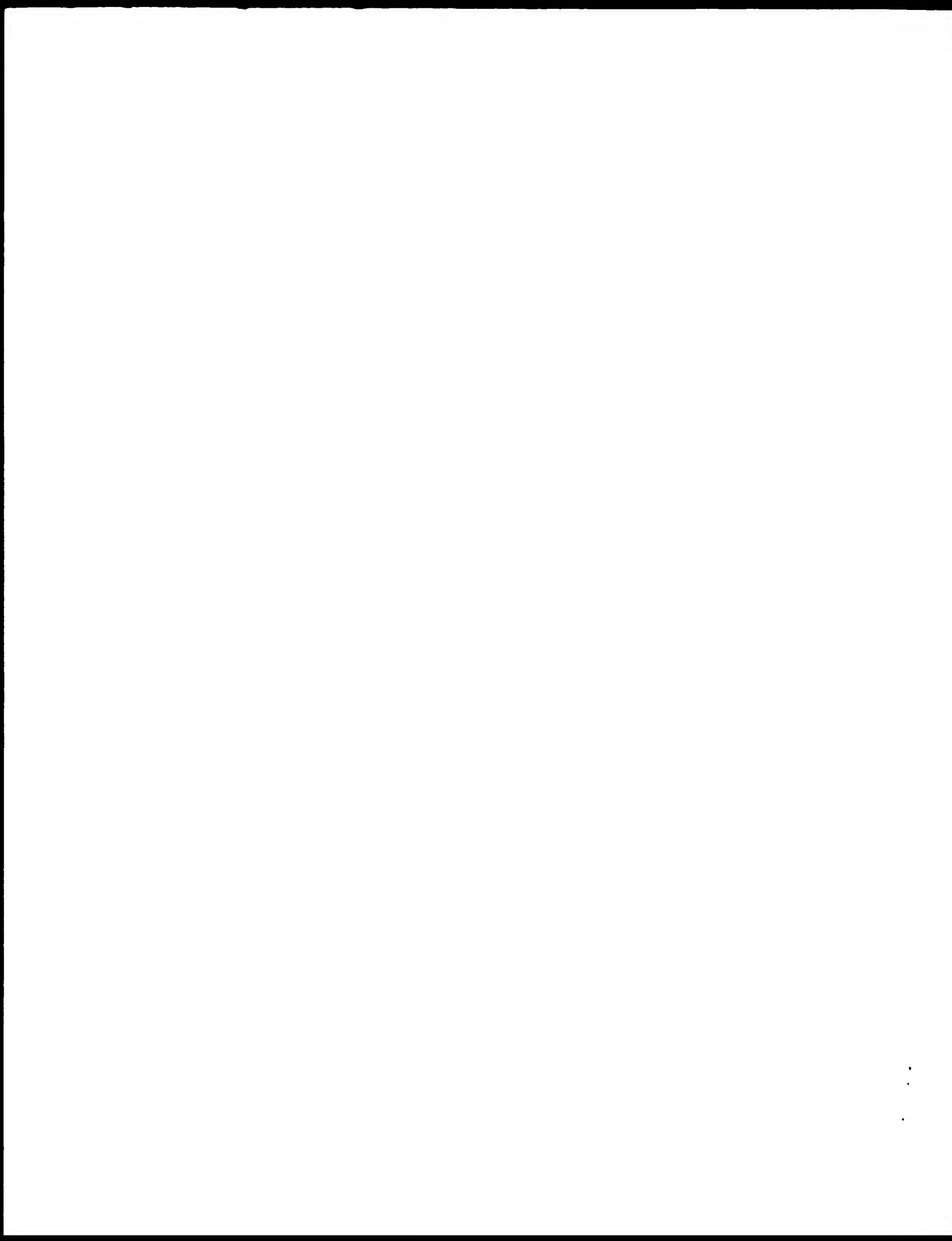
XX (HARD) HARVARD COLLEGE.

XX (HARD) UNIV HARVARD

XX Jones DL, Munger K;

DR WP1: 2000-587315/55
 DR N-PSDB: AAA96020
 XX Protein and nucleic acid compositions for preventing and treating
 PT neoplasias (particularly cancer); comprises a novel chimeric cyclin
 PT dependent kinase inhibitor and adenovirus E4 protein -
 XX
 XX Example 1: Page 122; 126pp; English.
 CC This sequence represents the human p27 protein.
 CC The invention relates to a protein composition comprising a novel
 CC purified chimeric cyclin dependent kinase inhibitor (CDKi) and a
 CC purified adenovirus E4 protein. The compositions comprising the protein,
 CC or the DNA encoding it are useful for treating neoplasias in animals. The
 CC compositions also find use in assays to eliminate a specific
 CC sub-population of cultured cells, to determine the susceptibility of
 CC neoplastic cells to treatment with the compositions and also in assays to
 CC synchronise cell growth in cultured cells.
 XX
 XX Sequence 198 AA:
 CC
 CC Query Match 100.0% Score 383; DB 21; Length 198;
 CC Best Local Similarity 100.0%; Pred No 9 4e-41;
 CC Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EHPKPSACNLPFGPVDFHEELTRQIFKHCQDMFEASQPKWNDFONHKPLDGKYEWEVEK 60
 Db 22 EHPKPSACNLPFGPVDFHEELTRQIFKHCQDMFEASQPKWNDFONHKPLDGKYEWEVEK 81
 QY 61 GSLPEFY 67
 Db 82 GSLPEFY 88
 CC
 CC RESULT 12
 CC AAY96052
 ID AAY96052 standard; Protein: 198 AA.
 AC AAY96052,
 XX 05-DEC-2000 (first entry)
 DE Human cyclin dependent kinase inhibitor p27
 XX
 XX Cyclin dependent kinase inhibitor; CDKi; CIP; KIP; human; p27;
 KW smooth muscle cell; restenosis; vasotrophic; antiproliferative;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Domain 25..93
 FT /note= "CDK inhibitory domain"
 FT Domain 144..194
 FT /note= "Q1 domain"
 FT Peptide 152..166
 FT /note= "nuclear localisation signal"
 FT Modified-site 10..13
 FT /note= "O-phosphorylated, weak CDK phosphorylation site"
 FT Modified-site 178..181
 FT /note= "O-phosphorylated, phosphorylation site for
 FT proline-directed kinases"
 FT Modified-site 187..190
 FT /note= "O-phosphorylated; CDK phosphorylation consensus site"
 FT
 XX
 PN W0200052159-A1.
 XX
 PD 08-SEP-2000.
 XX
 XX 28-FEB-2000; 2000WO US04971.

DR 01 MAR 1999; 99US 0122974.
 DR 05-NOV-1999; 99US-0163682.
 PR 04-DEC-1999; 99US-0457568.
 XX (CELL-) CELL GENESYS INC.
 PA (MITO-) MITOTIX INC.
 XX
 XX McArthur J, Gyuris J, Finer M;
 DR WP1: 2000-584183/56
 DR N-PSDB: AAA50499.
 XX N-erbB recombination activates for inhibiting proliferation of smooth
 PT muscle cells in a restenosis, is replication deficient and comprises
 PT a transgene encoding a cyclin dependent kinase inhibitor -
 XX
 XX Example 1: Page 119-120; 126pp; English.
 CC The present sequence is that of human p27, a cyclin dependent
 CC kinase inhibitor (CDKi) that inhibits smooth muscle cell
 CC proliferation. A claimed method for inhibiting smooth muscle cell
 CC hyperproliferation involves transducing smooth muscle cells with a
 CC replication-deficient recombinant adenovirus that lacks a functional
 CC E1 region and a functional E4 region, and comprises a transgene
 CC encoding a CDKi. The CDKi is selected from an INK4 family protein
 CC such as human p16, a CIP/KIP family protein such as p27, active
 CC fragments of these, or fusion proteins comprising active fragments
 CC of an INK4 family protein and a CIP/KIP family protein (see AAY96046
 CC and AAY96049). The method is used to inhibit mammalian smooth muscle
 CC cell hyperproliferation induced by injury caused by angioplasty,
 CC stent placement or vein engraftment. It is useful for treating
 CC vascular pathologies, e.g. restenosis. Also claimed are recombinant
 CC lentiviruses encoding CDKis.
 XX
 XX Sequence 198 AA:
 CC
 CC Query Match 100.0% Score 383; DB 21; Length 198;
 CC Best Local Similarity 100.0%; Pred No 9 4e-41;
 CC Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EHPKPSACNLPFGPVDFHEELTRQIFKHCQDMFEASQPKWNDFONHKPLDGKYEWEVEK 60
 Db 22 EHPKPSACNLPFGPVDFHEELTRQIFKHCQDMFEASQPKWNDFONHKPLDGKYEWEVEK 81
 QY 61 GSLPEFY 67
 Db 82 GSLPEFY 88
 CC
 CC RESULT 13
 CC AAY96066
 ID AAY96066 standard; Protein: 198 AA.
 AC AAY96066;
 XX 05-DEC-2000 (first entry)
 DE Human cyclin dependent kinase inhibitor p27.
 XX
 XX Cyclin dependent kinase inhibitor; CDKi; CIP; KIP; human; p27;
 KW angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;
 KW endometriosis, psoriasis, vascular retinopathy, cytostatic,
 KW antiarthritic, antiheumatic, gynaecological, antipsoriatic,
 KW antiproliferative; gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Domain 25..93
 FT /note= "CDK inhibitory domain"
 FT Domain 144..194
 FT /note= "Q1 domain"
 FT Peptide 152..166



Genome version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

For: 300 May 30, 2003 22:55:27 (without alignments)
392,644 Million cell updates/sec

Title: US-09-865-018b-2_copy_22_88

Percent score: 383

Sequence: 1 EHPKPSACRNLFSPVDHEEL... PLECKYEWQWFKGSLPEFY 57

Scoring table: BLOSUM62

Gap: 10 0 , Gapext 0 5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued_Patents_AA*

- 1: /seq2/6/ptdata/1/seq/5A_00MB.pep.*
- 2: /seq2/6/ptdata/1/seq/5A_00MB.pep.*
- 3: /seq2/6/ptdata/1/seq/5A_00MB.pep.*
- 4: /seq2/6/ptdata/1/seq/5A_00MB.pep.*
- 5: /seq2/6/ptdata/1/seq/5A_00MB.pep.*
- 6: /seq2/6/ptdata/1/seq/5A_00MB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	383	100.0	177	4	US-09-457-568-12
2	383	100.0	177	4	US-09-457-568-12
3	383	100.0	198	1	US-08-275-983B-3
4	383	100.0	198	1	US-08-406-248-4
5	383	100.0	198	4	US-08-897-333A-2
6	383	100.0	198	4	US-09-240-906-6
7	383	100.0	198	4	US-08-794-002-2
8	383	100.0	198	4	US-09-457-568-26
9	383	100.0	198	4	US-09-457-568-26
10	383	100.0	334	4	US-09-457-568-16
11	383	100.0	334	4	US-09-457-568-16
12	383	100.0	348	4	US-09-457-568-14
13	383	100.0	348	4	US-09-457-568-14
14	383	100.0	465	4	US-09-457-568-6
15	383	100.0	465	4	US-09-457-568-10
16	383	100.0	465	4	US-09-457-568-6
17	383	100.0	465	4	US-09-457-568-10
18	383	100.0	380	4	US-09-457-568-8
19	383	100.0	380	4	US-09-457-568-8
20	383	100.0	391	4	US-08-540-941-2
21	383	100.0	391	4	US-09-457-568-4
22	383	100.0	391	4	US-09-457-568-4
23	383	100.0	391	4	US-09-457-568-4
24	383	100.0	391	4	US-08-854-0398-2
25	383	100.0	391	4	US-08-854-0398-2
26	383	100.0	391	4	US-08-854-0398-2
27	383	100.0	391	4	US-08-854-0398-2

Sequence 4, Appli
Sequence 4, Appli
Sequence 30, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 56, Appl
Sequence 50, Appl
Sequence 53, Appl
Sequence 52, Appl
Sequence 49, Appl
Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-457-568-12
Sequence 12, Application US/09457568
Patent No. 6413943

GENERAL INFORMATION:

APPLICANT: McArthur, James G

APPLICANT: Gyuris, Jen

APPLICANT: Finer, Mitchell H

TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of

FILE REFERENCE: 106482.091

CURRENT APPLICATION NUMBER: US/09/457,568

EARLIER FILING DATE: 1999-12-09

EARLIER APPLICATION NUMBER: 60/122,974

EARLIER FILING DATE: 1999-03-01

EARLIER APPLICATION NUMBER: 60/163,082

EARLIER FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Parent In Ver. 2.0

SEQ ID NO 12

LENGTH: 177

TYPE: PRT

ORGANISM: Homo sapiens

US-09-457-568-12

Query Match 100.0%; Score 383; DB 4; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.3e-41;

Matches 67, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

Qy 1 EHPKPSACRNLFSPVDHEELTRLEKHCPCMEASQPKWNFTQNHKPLPGKYEWQWVEK 60

Lb 22 EHPKPSACRNLFSPVDHEELTRLEKHCPCMEASQPKWNFTQNHKPLPGKYEWQWVEK 81

Qy 61 GSLPEFY 67

Lb 82 GSLPEFY 88

RESULT 2

US-09-457-568-12

Sequence 12, Application US/09457568

Patent No. 6420345

GENERAL INFORMATION:

APPLICANT: Patel, Salil D

APPLICANT: McArthur, James G

APPLICANT: Gyuris, Jen

TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of

FILE REFERENCE: 106482.287

CURRENT APPLICATION NUMBER: US/09/457,568


```

: TITLE OF INVENTION: METHOD FOR TREATING VASCULAR PROLIFERATIVE DISEASES
: FILE REFERENCE: 8642/4
: CURRENT APPLICATION NUMBER: US/08/937,333A
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 2
: LENGTH: 198
: TYPE: PRT
: ORGANISM: Homo sapiens
US-08-897-333A-2

Query Match 100.0% Score 383; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.5e-41;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHKPSACNLFQGVDPHEFLTRLEKHCPTMFEASQPKWNFDQNHKPLEGKYEWQVEVK 60
|||||
DB 22 EHKPSACNLFQGVDPHEFLTRLEKHCPTMFEASQPKWNFDQNHKPLEGKYEWQVEVK 81

QY 61 GSLPEFY 67
|||||
DB 82 GSLPEFY 88

RESULT 6
US-09-240-906-6
: Sequence 6, Application US/09240906
: Patent No. 6245965
: GENERAL INFORMATION:
: APPLICANT: ROUSSEL, MARTINE F.
: APPLICANT: SNEYNE, RICHARD
: APPLICANT: ZINDY, FREDERIQUE
: APPLICANT: CUNNINGHAM, JUSTINE
: TITLE OF INVENTION: CELLS THAT LACK P19INK4D AND P27KIP1 ACTIVITY AND
: TITLE OF INVENTION: METHODS OF USE THEREOF
: FILE REFERENCE: 1340-1-025
: CURRENT APPLICATION NUMBER: US/09/240-906
: CURRENT FILING DATE: 1999-01-29
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 6
: LENGTH: 198
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-240-906-6

Query Match 100.0% Score 383; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.5e-41;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHKPSACNLFQGVDPHEFLTRLEKHCPTMFEASQPKWNFDQNHKPLEGKYEWQVEVK 60
|||||
DB 22 EHKPSACNLFQGVDPHEFLTRLEKHCPTMFEASQPKWNFDQNHKPLEGKYEWQVEVK 81

QY 61 GSLPEFY 67
|||||
DB 82 GSLPEFY 88

RESULT 7
US-08-794-002-2
: Sequence 2, Application US/08794002
: Patent No. 6316208
: GENERAL INFORMATION:
: APPLICANT: Roberts, James M.
: APPLICANT: Porter, Peggy L.
: TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHODS FOR ITS
: TITLE OF INVENTION: PRODUCTION AND USE
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FOLEY, HOAG & ELLIOT LLP

```

```

: STREET: One Post Office Square
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109 2170
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/794,002
: FILING DATE: 03-FEB-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Vincent, Matthew P.
: REGISTRATION NUMBER: 36,709
: REFERENCE/DOCKET NUMBER: MIV-079,03
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-842-1000
: TELEFAX: 617-832-7000
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 198 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-794-002-2

Query Match 100.0% Score 383; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.5e-41;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHKPSACNLFQGVDPHEFLTRLEKHCPTMFEASQPKWNFDQNHKPLEGKYEWQVEVK 60
|||||
DB 22 EHKPSACNLFQGVDPHEFLTRLEKHCPTMFEASQPKWNFDQNHKPLEGKYEWQVEVK 81

QY 61 GSLPEFY 67
|||||
DB 82 GSLPEFY 88

RESULT 8
US-09-457-568-26
: Sequence 26, Application US/09457568
: Patent No. 6413943
: GENERAL INFORMATION:
: APPLICANT: McArthur, James G
: APPLICANT: Gyuris, Jeno
: APPLICANT: Finer, Mitchell H
: TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
: TITLE OF INVENTION: Smooth Muscle Cells
: FILE REFERENCE: 196482, 691
: CURRENT APPLICATION NUMBER: US/09/457,568
: CURRENT FILING DATE: 1999-12-09
: EARLIER APPLICATION NUMBER: 60/122,974
: EARLIER FILING DATE: 1999-03-01
: EARLIER APPLICATION NUMBER: 60/163,682
: EARLIER FILING DATE: 1999-11-05
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 26
: LENGTH: 198
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-457-568-26

Query Match 100.0% Score 383; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.5e-41;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHKPSACNLFQGVDPHEFLTRLEKHCPTMFEASQPKWNFDQNHKPLEGKYEWQVEVK 60
|||||

```


Query Match 100.0%; Score 383; DB 4; Length 348;
Best Local Similarity 100.0%; Pred. No. 3.3e-41;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACNLFPGVDHEELTRDLEKHCRCMEASQKKNWFDQNHKPLEGKYEWQVEVK 80
|||||
DB 22 EHPKPSACNLFPGVDHEELTRDLEKHCRCMEASQKKNWFDQNHKPLEGKYEWQVEVK 81
|||||

QY 61 GSLPEFY 67
|||||

DB 82 GSLPEFY 88
|||||

RESULT 13
US-09-457-568-14
; Sequence 14, Application US/09457568
; Patent No. 6413943
; GENERAL INFORMATION:
; APPLICANT: Patel, Salil D
; APPLICANT: McArthur, James G
; APPLICANT: Gyuris, Jeno
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
; FILE REFERENCE: 106482.287
; CURRENT APPLICATION NUMBER: US/09/457,568
; EARLIER FILING DATE: 1999-12-09
; EARLIER APPLICATION NUMBER: 60/122,974
; EARLIER FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 60/163,682
; EARLIER FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-568-14

Query Match 100.0%; Score 383; DB 4; Length 348;
Best Local Similarity 100.0%; Pred. No. 3.3e-41;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACNLFPGVDHEELTRDLEKHCRCMEASQKKNWFDQNHKPLEGKYEWQVEVK 80
|||||
DB 22 EHPKPSACNLFPGVDHEELTRDLEKHCRCMEASQKKNWFDQNHKPLEGKYEWQVEVK 81
|||||

QY 61 GSLPEFY 67
|||||

DB 82 GSLPEFY 88
|||||

RESULT 14
US-09-457-568-6
; Sequence 6, Application US/09457568
; Patent No. 6413943
; GENERAL INFORMATION:
; APPLICANT: McArthur, James G
; APPLICANT: Gyuris, Jeno
; APPLICANT: Finer, Mitchell H
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
; FILE REFERENCE: 106482.691
; CURRENT APPLICATION NUMBER: US/09/457,568
; EARLIER FILING DATE: 1999-12-09
; EARLIER APPLICATION NUMBER: 60/122,974
; EARLIER FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 60/163,682
; EARLIER FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 365
; TYPE: PRT

ORGANISM: Homo sapiens
US-09-457-568-6

Query Match 100.0%; Score 383; DB 4; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.3e-41;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACNLFPGVDHEELTRDLEKHCRCMEASQKKNWFDQNHKPLEGKYEWQVEVK 60
|||||
DB 32 EHPKPSACNLFPGVDHEELTRDLEKHCRCMEASQKKNWFDQNHKPLEGKYEWQVEVK 91
|||||

QY 61 GSLPEFY 67
|||||

DB 92 GSLPEFY 98
|||||

RESULT 15
US-09-457-568-10
; Sequence 10, Application US/09457568
; Patent No. 6413943
; GENERAL INFORMATION:
; APPLICANT: McArthur, James G
; APPLICANT: Gyuris, Jeno
; APPLICANT: Finer, Mitchell H
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
; FILE REFERENCE: 106482.691
; CURRENT APPLICATION NUMBER: US/09/457,568
; EARLIER FILING DATE: 1999-12-09
; EARLIER APPLICATION NUMBER: 60/122,974
; EARLIER FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 60/163,682
; EARLIER FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-568-10

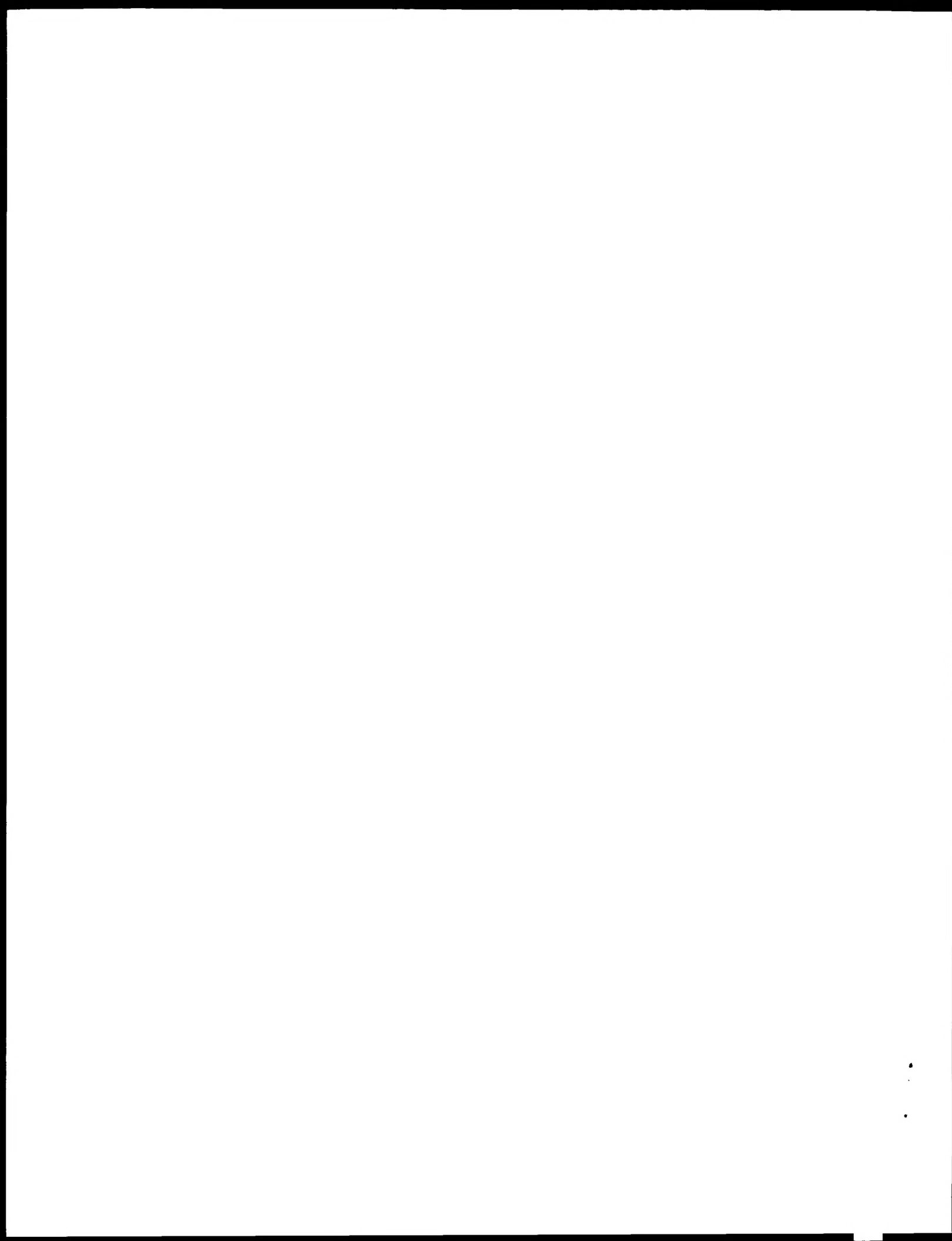
Query Match 100.0%; Score 383; DB 4; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.3e-41;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACNLFPGVDHEELTRDLEKHCRCMEASQKKNWFDQNHKPLEGKYEWQVEVK 60
|||||
DB 189 EHPKPSACNLFPGVDHEELTRDLEKHCRCMEASQKKNWFDQNHKPLEGKYEWQVEVK 248
|||||

QY 61 GSLPEFY 67
|||||

DB 249 GSLPEFY 255
|||||

Search completed May 30, 2003, 09:03:43
Job time : 6.02067 secs



GenCore version 5.1.6
Copyright (C) 1993 2003 Compugen Ltd

OM protein protein search, using sw model

Run on: May 30, 2003, 08:54:42 : Search time: 629.62 seconds
(without alignments)
1144.739 Million cell updates/sec

Title: US-09-865-018b-2_copy_22_88

Perfect score: 383
Sequence: 1 EHPKPSACRNLFQVDFEEL... PLEKYPWQFVEKSTPEFY 67

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 28224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283234

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIP-731*

1: pir1*

2: pir2*

3: pir3*

4: pir4*

Prod. No. is the number of results predicted by search to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	380	96.2	198	2	152718
2	369	96.3	197	2	149064
3	182	47.5	316	2	924234
4	178	46.5	210	2	151683
5	174	45.4	348	2	149262
6	160	41.8	164	2	184725
7	153	39.9	181	2	188674
8	151	39.4	181	2	154380
9	146	38.1	159	2	149023
10	143	37.3	143	2	A49438
11	121.5	31.7	258	2	T34499
12	100	26.1	191	2	T01132
13	88.5	24.1	184	2	T24436
14	70.5	18.4	196	2	T09968
15	69.5	18.1	470	2	S50383
16	69	14.0	196	2	H96532
17	68.5	17.9	209	2	T46140
18	68.5	17.9	611	1	S12566
19	67.6	17.6	246	1	S49770
20	67.5	17.6	489	2	S63431
21	66	17.2	327	2	T30797
22	66	17.2	885	2	138968
23	65.5	17.1	382	1	G01589
24	65	17.0	671	1	OKBOG
25	65	17.0	686	1	S05702
26	65	17.0	903	2	T20884
27	64.5	16.8	570	1	A36954
28	64	16.7	317	2	G73863
29	63.5	16.6	533	2	S52046

30	62	16.2	1094	2	S49313
31	61.5	16.1	279	2	T21666
32	61.5	16.1	380	2	S66728
33	61.5	16.1	633	2	T28788
34	61	15.9	564	2	F87305
35	60.5	15.8	787	2	A72230
36	60.5	15.8	1557	2	T18412
37	60	15.7	153	2	E85850
38	60	15.7	245	2	A82576
39	60	15.7	450	1	A43733
40	60	15.7	1211	2	S65799
41	59.5	15.5	149	2	E69667
42	59.5	15.5	284	2	S37680
43	59.5	15.5	573	2	F94560
44	59.5	15.5	732	2	T40861
45	59	15.4	120	2	AB1425

ALIGNMENTS

RESULT 1

152718

gene p27Kip1 protein - human

C:Species: Homo sapiens (man)

C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000

C:Accession: 152718

R:Pieterpol, J.A., Richlander, S.K., Sato, Y., Papadopoulos, N.; Liu, R.; Friedman, C.

Cancer Res. 55, 1206-1210, 1995

A>Title: Assignment of the human p27Kip1 gene to 12p13 and its analysis in leukemias.

A:Reference number: 152718, M01D:95188144; PMID:7882309

A:Accession: 152718

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-198 <RES>

A:Cross-reference: 58 S70388, NID:608482, IILN AA:14-41.1, FID:84261944

C:Genetics:

A:Gene: p27Kip1

A:Introns: 159/1

Query Match 99.2%, Score 380, DB 2, Length 198.

Best Local Similarity 98.5%; Pred. No. 8.9e-36;

Matches 66, Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACRNLFQVDFEELTFLFKHPTMFESAKKNFQFNHKKPIEKYEWQVEK 60

DL 22 LHPKPSACRNLFQVDFEELTFLFKHPTMFESAKKNFQFNHKKPIEKYEWQVEK 81

QY 61 GSLPEFY 67

DL 82 GSLPEFY 88

RESULT 2

149064

cyclin-cdk inhibitor p27 - mouse

N:A:termed names: cdi p27, G1 cyclin cyclin-dependent kinase inhibitor p27

C:Species: Mus musculus (house mouse)

C>Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 05-Nov-1999

C:Accession: 149064

R:Toyoshima, H.; Hunter, T.

Cell 78, 67-74, 1994

A>Title: p27, a novel inhibitor of G1 cyclin-cdk protein kinase activity, is related

A:Reference number: A4459, M01D:9406614; PMID:843423

A:Accession: 149064

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-197 <RES>

A:Cross-reference: ILM:010446, NID:9532771, IILN AAA21144.1, FID:9532772

C:Keywords: cell cycle control

Query Match 96.3%, Score 269, DB 2, Length 197;

Best Local Similarity 94.0%, Pred. No. 1.6e-34,

[illegible]

Query Match	38.1%	Score	146,	DB	2,	Length	159,
Best Local Similarity	40.6%	Pred. No.	2.6e-08;				
Matches	26;	Conservative	10;	Mismatches	28;	Indels	0;
						Gaps	0;

4	KPSACRNLFQVDFHEELTRULEKHCROMEASQKKNWDFQNHKPLGKGYEQWQVEKXSL	63
18	PSKVCWFLFQVDFHDSQILPRDCLDALMAGLCQAPRWNFDFVTFLEGNFVWEPVRSGL	72

54	PEPY	57
73	PKVY	76

```

RESULT 10
A49438
p53 tumor suppression mediator WAF1 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C:Accession: A49438
P:Cell: Delt1, W.S.; Tokino, T.; Vandeulsen, V.E.; Levy, D.B.; Parsons, P.; Trent
Cell 75, 817-825, 1993
A:Title: WAF1, a potential mediator of p53 tumor suppression.
A:Reference number: A49438; MIM:604752; PMID:824752
A:Accession: A49438
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-143 <E1>
A:Note: sequence extracted from NCBI database (NCBI:140807, NCBI:140808)

```

4 KPSADNLGPGVDEHEELTFDLEKHCFDMEEASQPKWNEDFNHKKPLBGGKYWEVEVERKSL 63

13 RSKVWCLFENFDISESGKIALMAQLLQAGRWNFQVTEGLGFNFWYERVFSSJAL 72

1. $\frac{1}{2} \log 2$
 2. $\frac{1}{2} \log 2$
 3. $\frac{1}{2} \log 2$
 4. $\frac{1}{2} \log 2$
 5. $\frac{1}{2} \log 2$
 6. $\frac{1}{2} \log 2$
 7. $\frac{1}{2} \log 2$
 8. $\frac{1}{2} \log 2$
 9. $\frac{1}{2} \log 2$
 10. $\frac{1}{2} \log 2$

[illegible][illegible]

Journal of Interpersonal Violence, 20(1), 67-89.

C.Data: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 20-Jun-2000
 C.Accession: S50083
 R.Kato Jr., T. Ito, T. Ayaki, H. Ishizaki, K. Morita, T. Mitra, S. Ikenaga, M. Nucleic Acids Res. 22, 4119-4124, 1994
 A>Title: Cloning of a marsupial DNA photolyase gene and the lack of related nucleotide s
 A.Reference number: S50083; M01105;U23174; PM107937136
 A.Accession: S50083
 A>Status: preliminary
 A.Molecule type: mRNA
 A.Residues: 1-470 <A>
 A.Cross-references: EMBL:D319662; NID:gboln02; PIRN:HA00709 1; PDB:gp02750
 C.Superfamily: deoxyribodipyrimidine photo-lyase

```

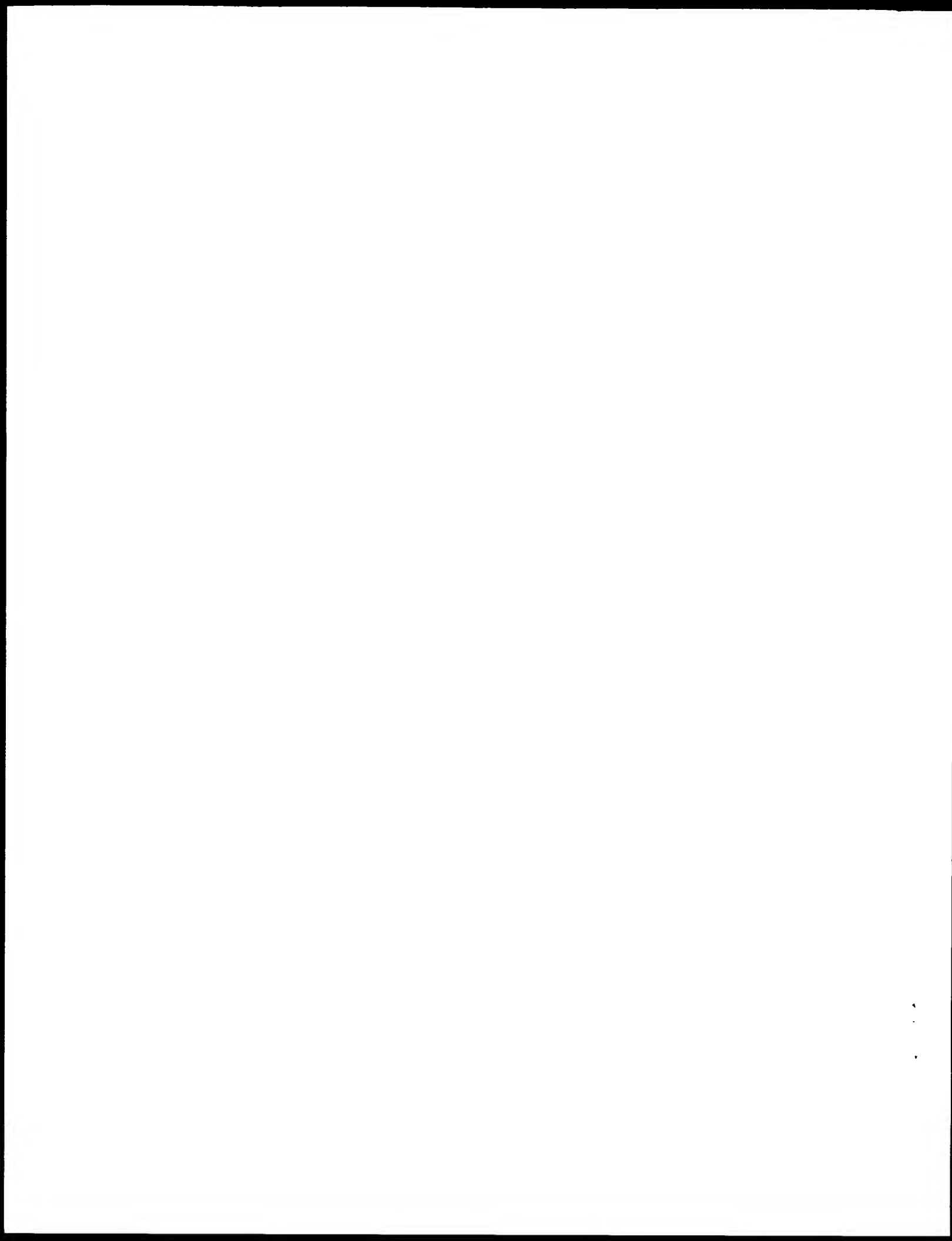
Query Match      18.18; Score 69.5; DB 2; Length 470,
Best Local Similarity 28.18; Prd. No. 4.5;
Matches 25; Conservative 11; Mismatches 30; Indels 23; Gaps 5;

QY      2 HPKPSACRNLT-----EGPVDHEELTRDLEKH-----CRDMEEAQSRKW---NDFD-- 43
      :|: ||| ||| :|: ||| :|: ||| :|: |||
Db      262 NPNKATLSNLSPEWHEGCVSVQKALEVQHKRSYPSVANFVEEAIVRELADNCFYN 321

QY      44 QNHKPLEGKYEQWQEV-----EKGSLPEFY 67
      :|: ||| ||| :|: |||
Db      322 KNVDKLEGAYDMAQTTLRLHAKDKKRPPLY 350

```

Search completed: May 30, 2003, 09:02:41
Job time : 7.62662 secs



GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 08:52:42 : Search time 28.659 seconds
(without alignments)
972.808 Million cell updates/sec

Title: US-09-865-018b-2_COPY_22_88
Perfect score: 383
Sequence: 1 BHPKPSACRNLFPGVDHEEL.....PLEGKYEMQEVKGLSLEPY 67

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum db seq length: 0

Maximum db seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	383	100.0	198	1	CDNB_HUMAN
2	372	97.1	198	1	CDNB_FELCA
3	369	96.3	197	1	CDNB_MOUSE
4	364	95.0	198	1	CDNB_CRTRP
5	360	94.0	178	1	CDNB_MGSLV
6	342	91.5	178	1	CDNB_HUMAN
7	342	91.5	178	1	CDNB_MOUSE
8	342	91.5	178	1	CDNB_HUMAN
9	342	91.5	178	1	CDNB_MOUSE
10	342	91.5	178	1	CDNB_FELCA
11	342	91.5	178	1	CDNB_MOUSE
12	342	91.5	178	1	CDNB_MOUSE
13	342	91.5	178	1	CDNB_MOUSE
14	342	91.5	178	1	CDNB_MOUSE
15	342	91.5	178	1	CDNB_MOUSE
16	342	91.5	178	1	CDNB_MOUSE
17	342	91.5	178	1	CDNB_MOUSE
18	342	91.5	178	1	CDNB_MOUSE
19	342	91.5	178	1	CDNB_MOUSE
20	342	91.5	178	1	CDNB_MOUSE
21	342	91.5	178	1	CDNB_MOUSE
22	342	91.5	178	1	CDNB_MOUSE
23	342	91.5	178	1	CDNB_MOUSE
24	342	91.5	178	1	CDNB_MOUSE
25	342	91.5	178	1	CDNB_MOUSE
26	342	91.5	178	1	CDNB_MOUSE
27	342	91.5	178	1	CDNB_MOUSE
28	342	91.5	178	1	CDNB_MOUSE
29	342	91.5	178	1	CDNB_MOUSE
30	342	91.5	178	1	CDNB_MOUSE
31	342	91.5	178	1	CDNB_MOUSE
32	342	91.5	178	1	CDNB_MOUSE
33	342	91.5	178	1	CDNB_MOUSE

34	58.5	15.3	724	1	VG01_BDP22	p26744 bacterioph
35	58.5	15.3	804	1	PPN6_YEAST	p32786 saccharomyc
36	58.5	15.3	942	1	15P2_HUMAN	p32019 homo sapien
37	58	15.1	382	1	VATH_DROME	q4v4j1 drosophila
38	58	15.1	761	1	RIR1_BUCAI	p57276 buchmera ap
39	58	15.1	834	1	CASL_HUMAN	q14511 homo sapien
40	58	15.1	2186	1	YL52_CAFEL	p34431 caenorhabdi
41	57.5	15.0	376	1	SPH_STIPPY	p00470 streptococc
42	57.5	15.0	490	1	TIME_ECOLI	q47282 escherichia
43	57.5	15.0	525	1	NAB2_YEAST	p32505 saccharomyc
44	57.5	15.0	740	1	CATA_MYCHO	p46817 mycobacteri
45	57.5	15.0	740	1	CATA_MYCIU	q08129 mycobacteri

ALIGNMENTS

RESULT 1	CDNB_HUMAN	STANDARD;	PRT;	198 AA.
AC	P46527	Q15437;		
DT	01-NOV-1995	(Rel. 32, Created)		
DT	01-NOV-1995	(Rel. 32, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase inhibitor p27) (p27Kip1).			
GN	CDKN1B OR KIP1			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
PP	SEQUENCE FROM N.A., AND SEQUENCE OF 28-79 AND 104-152.			
PC	TISSUE=Kidney;			
RX	MEDLINE=94306518; PubMed=8033212;			
PA	Polyak K , Lee M-H , Erdjument-Bromage H , Koff A , Roberts I M ,			
PA	Tempst P., Massague J.;			
RT	"Cloning of p27Kip1, a cyclin-dependent kinase inhibitor and a			
RT	potential mediator of extracellular antimetogenic signals.";			
PL	Cell 78:59-66(1994).			
PN	[2]			
PP	SEQUENCE FROM N.A.			
PP	MEDLINE=95184144; PubMed=7882109;			
PA	Pietenpol J.A., Bohlender S.K., Sato Y., Papadopoulos N., Liu R.,			
PA	Piedraza C., Trask P.J., Roberts I.M., Kinzler K.W., Rowley T.D.;			
RT	"Assignment of the human p27Kip1 gene to 12p13 and its analysis in			
RT	leukemias.";			
PL	Cancer Res. 55:1206-1210(1995).			
PN	[3]			
PP	SEQUENCE FROM N.A., AND VARIANTS TYP-15 AND GLY-109.			
PA	Rieder M.J., Braun A.C., Montoya M.A., Chung M.W., Nguyen C.P.,			
PA	Nguyen D.A., Livingston P.J., Poel C.L., Robertson P.D.,			
PA	Schackwitz W.S., Sherwood J.K., Wittrak T.A., Nickerson D.A.;			
PL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
PN	(4)			
PP	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 23-106 OF COMPLEX WITH CDK2			
PP	AND CC2A.			
PP	MEDLINE=96300318; PubMed=8684460;			
PA	Russo A.A., Jeffrey P.D., Patten A.K., Massague J., Pavletich N.P.;			
RT	"Crystal structure of the p27Kip1 cyclin dependent-kinase inhibitor			
RT	bound to the cyclin A-Cdk2 complex.";			
PL	Nature 392:363-367(1999)			
CC	FUNCTION: Involved in G1 arrest. May mediate TGF beta-induced G1			
CC	arrest. Binds to and inhibits complexes formed by cyclin E-CDK2,			
CC	cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin			
CC	NUP50 is required for nuclear import and for degradation of			
CC	phosphorylated p27Kip1 after nuclear import (By similarity).			
CC	SUBUNIT: Interacts with NUP50 (By similarity).			
CC	TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES TESTED. HIGHEST			
CC	LEVELS IN SKELETAL MUSCLE, LOWEST IN LIVER AND KIDNEY			
CC	NOTE: A FEW OF THE SEQUENCES CONTAINING ONLY AA 28-79 RETAINS			
CC	SUBSTANTIAL KIP1 CYCLIN A/CDK2 INHIBITORY ACTIVITY.			


```

MEDLINE=95247028; PubMed 7729644.
RA Matsuoka S., Edwards M.C., Bai C., Parker S., Zhang P., Baldini A ,
FA Harper J.W., Elledge S.J.;
RT "p53/KIP2, a structurally distinct member of the p21Cip1 Cdk inhibitor
PT family, is a candidate tumor suppressor gene.";
RL Genes Dev. 9:650-662(1995).
CC -- FUNCTION: POTENT TIGHT-TIGHT-BINDING INHIBITOR OF SEVERAL CDK/CDK
CC COMPLEXES (CYCLIN E+CDK2, CYCLIN D2+CDK4, AND CYCLIN A+CDK2) AND,
CC TO LESSER EXTENT, OF THE MITOTIC CYCLIN B+CDK2. NEGATIVE REGULATOR
CC OF CELL PROLIFERATION MAY PLAY A ROLE IN MAINTENANCE OF THE
CC NONPROLIFERATIVE STATE THROUGHOUT LIFE.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: IT IS EXPRESSED IN THE HEART, BRAIN, LUNG,
CC SKELETAL MUSCLE, KIDNEY, PANCREAS AND TESTIS. HIGH LEVELS ARE SEEN
CC IN THE PLACENTA WHILE LOW LEVELS ARE SEEN IN THE LIVER.
-----
CC This SWISS-Prot entry is copyright © It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/aboutus/ or
CC or send an email to license@sib-sb.ch).
-----
CC EMBL: U20553; AAC2186.1; -
CC FBL: U22399; AAA85096.1; -
CC MGI: 104564; Gdnlc.
CC InterPro: IPR031475; CDI.
CC Pfam: PF02234; CDI; 1.
CC Cell cycle; Alternative splicing.
CC DOMAIN 108 189 PRO-RICH.
CC FT DOMAIN 178 284 GLU/ASP-RICH.
CC FT DOMAIN 309 312 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC FT VARSPLOC 1 13 MISSING (IN ISOFORM KIP2R/P47B)
CC FT CONFLICT 150 151 DA -> EP (IN REF. 2).
CC SQ SEQUENCE 348 AA; 47331 MW; 10A8538D77016D9 CRC64;

Query Match 45.4%; Score 174; DR 1; Length 348;
Best Local Similarity 47.0%; Pred.No. 5,6e-12;
Matches 31; Conservative 12; Mismatches 21; Indels 2; Gaps 1;

QY 4 KPSACNPLGGPVTHEELTPELEKHCKHMEASQKKWNEFONHKPLE--CKVEPWQVPKG 61
Db : ||||| ||||||| ||| : | ||:|| | | | | | | |
28 RSSACSLFGPGVTHFGFLGFELPMFLAEI NAFTCNPNWFNFGLGVLPVP3PQLQWMEVUSE 87

QY 62 SLPEFY 67
Db | | |
88 SVPAFY 93

RESULT 8
CONL_HUMAN STARGARD, PRT, 164 AA.
ID GNLI_HUMAN AC P38936; Q9RUT4;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cyclin-dependent kinase inhibitor 1 (p21) (CDK-interacting protein 1)
DE (Melanoma differentiation associated protein 6) (MDA-6).
GN CDKNIA OR CDKN1 OR Cip1 OR Waf1 OR Mas6 OR Smi1 OR P21 OR CAP20
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homin
OX NCBI_Taxid:9606;
RN [1]
RR SEQUENCE FROM N.A.
RX MEDLINE=94041946; PubMed=9242751;
RA Harper J.W., Adami G.R., Wei N., Keyomarsi K., Ellledge S.J.;
RT "The p21 Cdk interacting protein Cip1 is a potent inhibitor of cll
PT cyclin-dependent kinases."
RL Cell 75:805-816(1993).
RN [2]
RR SEQUENCE FROM N.A.
```


DT 21-JUL-1986 (rel. 01, last sequence update)
DT 15-JUN-2002 (rel. 41, last annotation update)
DE cGMP-dependent protein kinase I, alpha isozyme (EC 2.7.1.37) (cGK I
DE alpha) (CGK1-alpha).
GN PRKGI OR PPKGPIA
OS Bos taurus (Bovine).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eumetazoa; Cetartiodactyla; Kuminantia; Pecora; Bovidae;
CC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SPQINFNT PPOM N A
RX MEDLINE=89325663; PubMed=2548620;
RA Wernet W., Fluckerz V., Hofmann F.
RT "The cDNA of the two isoforms of bovine cGMP-dependent protein
RT kinase.";
RL FEBS Lett. 251:191-196(1989)
RN [2]
RX SEQUENC OF 1117, 89 374 AND 407-676.
RA MEDLINE=85073407; PubMed=6001741;
RA Takio K., Wade R.D., Smith S.R., Krebs E.G., Walsh K.A., Titani K.;
RT "Guanosine cyclic 3',5'-phosphate-dependent protein kinase, a
RT chimeric protein homologous with two separate protein families.";
RL Biochemistry 23:4207-4218(1984).
RN [3]
RX SEQUENCE OF 13-104.
RA MEDLINE=83213511; PubMed=6304091;
RA Takio K., Smith S.R., Walsh K.A., Krebs E.G., Titani K.;
RT "Amino acid sequence around a 'hinge' region and its
RT 'autophosphorylation' site in bovine lung cGMP-dependent protein
RT kinase.";
RL J. Biol. Chem. 258:5531-5536(1983).
RN [4]
RX SEQUENCE OF 373-409.
RA MEDLINE=82098123; PubMed=6274962;
RA Hashimoto E., Takio K., Krebs E.G.;
RT "Amino acid sequence at the ATP-binding site of cGMP-dependent
RT protein kinase.";
RL J. Biol. Chem. 257:727-733(1982).
RN [5]
RX SEQUENCE OF 78-81, AND CHARACTERIZATION.
RA MEDLINE=84029406; PubMed=2822399;
RA Heil W.G., Landgraf W., Hofmann F.;
RT "A catalytically active fragment of cGMP-dependent protein kinase.
RT Occupation of its cGMP-binding sites does not affect its
RT phosphotransferase activity.";
RL Eur. J. Biochem. 168:117-121(1987)
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated
CC -!- ENZYME REGULATION: BINDING OF cGMP TO CGK RESULTS IN ENZYME
CC ACTIVATION.
CC -!- SUBUNIT: Homodimer, antiparallel and monomer.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CGK1-ALPHA (SHOWN HERE) AND
CC CGK1-BETA (AC P21136); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- PIM: 65 kDa monomer is produced by proteolytic cleavage.
CC -!- MISCELLANEOUS: EXHIBIT A SUBSTRATE SPECIFICITY SIMILAR BUT NOT
CC IDENTICAL TO THAT OF cGK.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC cGMP SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 2 CYCLIC NUCLEOTIDE-BINDING DOMAINS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed, usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X10886; CAA34214.1;
DR PIR: A00619; OKBOG.
DR PIR: S05034; S05034.
DR HSP: P05132; IATP.
DR InterPro, IPR00719, Euk_pkinase.

DK InterPro: IPR000961; Pkinase_C.
DK InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR002374; cGMP_kin.
DR InterPro: IPR000595; cNMP_binding.
DR Pfam: PF00027; cNMP_binding; 2.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00433; Pkinase_C; 1.
DR PRINTS: PR0104; CGMPKINASE.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TK; 1.
DR SMART: SM00100; cNMP; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DK PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DK PROSITE: PS00088; cNMP_BINDING_1; 2.
DK PROSITE: PS00089; cNMP_BINDING_2; 2.
DK PROSITE: PS00042; cNMP_BINDING_3; 2.
KW Transferrase; Serine/threonine-protein kinase; App-binding;
KW cNMP-binding; Acetylation; Phosphorylation; Alternative splicing
FT INITIUMET 0 0
FT MOD_RES 1 1 ACETYLATION.
FT DISULFID 42 42 INTERCHAIN (WITH DIMER).
FT MOD_RES 58 58 PHOSPHORYLATION (AUTO-).
FT MOD_RES 72 72 PHOSPHORYLATION (AUTO-).
FT MOD_RES 84 84 PHOSPHORYLATION (AUTO-).
FT DOMAIN 1 101 DIMERIZATION.
FT NP_BIND 102 219 CGMP 1.
FT NP_BIND 220 340 CGMP 2.
FT DOMAIN 359 618 PROTEIN KINASE.
FT NP_BIND 365 373 ATP (BY SIMILARITY).
FT BINDING 389 389 ATP (BY SIMILARITY).
FT ACT_SITE 483 483 BY SIMILARITY.
FT SITE 77 78 CLEAVAGE.
SQ SEQUENCE 670 AA, 76287 MW, A8E37ACFE8A7557D CRC64;

Query Match 17.0%; Score 65; DB 1; Length 670;
Best Local Similarity 37.8%; Pred. No. 11;
Matches 17, Conservative 7; Mismatches 13; Indels 8; Gaps 3;

QY 24 LEKHCHOMEEASOKKWNF-----DFCNHKKPLECKYEMQVEKGS 63
Db 590 IKRLKRD--NPSEPLGNLKNVKTOKRWFEQ-FNWEGLRKGTL 631

Search completed: May 30, 2003, 08:59:07
Job time: 4.85659 secs

GenCore version 5.1.6
Copyright (c) 1993 2003 Compugen Ltd

OM protein: protein search, using sw model

Run on: May 30, 2003, 08:53:57, Search time: 11:486, Seconds
(without alignments) 1181.337 Million cell updates/sec

Title: US-09-865-018b-2_copy_22_88
Perfect score: 383
Sequence: 1 EHPKPSACENFGVVDHLL.....FILEVIEWLGVKSLPEAY 67

Scoring table: BLOSUM62

Gapop 10 0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

- 1: SP_TREMBL_21:*
- 2: sp_archaea:*
- 3: sp_bacteria:*
- 4: sp_fungi:*
- 5: sp_human:*
- 6: sp_invertebrate:*
- 7: sp_mammal:*
- 8: sp_mhc:*
- 9: sp_organellar:*
- 10: sp_phase:*
- 11: sp_plant:*
- 12: sp_proteob:*
- 13: sp_virus:*
- 14: sp_vertebrate:*
- 15: sp_unclassified:*
- 16: sp_rvirus:*
- 17: sp_bacteriopl:*
- 18: sp_archaeap:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	383	100.0	158	4	043806
2	384	100.0	198	4	Q9NYG6
3	383	100.0	198	4	Q9B0S6
4	380	99.2	198	4	Q96TF0
5	372	97.1	172	6	Q9RFA5
6	372	97.1	197	11	Q08769
7	372	97.1	197	11	Q35792
8	372	97.1	198	6	Q9BDC3
9	255.5	58.9	179	13	Q90YX4
10	178	46.5	210	13	Q91603
11	175	45.7	209	13	Q91646
12	174	45.4	335	11	Q91V06
13	160	41.8	164	11	Q64315
14	153	39.9	164	4	Q96LE1
15	151	39.4	181	4	Q14010
16	121.5	31.7	258	5	Q22198

17	111	29.0	259	5	Q906R5
18	100	26.1	191	10	Q04154
19	109	25.1	191	10	Q82909
20	91.5	23.9	253	5	Q9W202
21	88.5	23.1	184	5	Q22197
22	85	22.2	163	10	Q91V92
23	84	21.9	245	5	Q94536
24	84	21.9	255	5	Q91654
25	82	21.4	222	10	Q9FKB5
26	82	21.4	245	5	Q91668
27	80.5	21.0	192	10	Q9F538
28	80.5	21.0	196	10	Q9LJ15
29	80	20.9	189	10	Q9LRV0
30	79	20.6	156	10	Q91X16
31	77	20.1	286	10	Q94CM0
32	77	20.1	289	10	Q48446
33	77	20.1	299	16	Q8XNG5
34	73.5	19.2	204	15	Q9V929
35	73	19.1	647	5	Q9VC60
36	72	18.8	106	6	Q77670
37	70.5	18.4	196	10	Q48597
38	69.5	18.1	470	6	Q28464
39	69	18.0	195	10	Q9FX90
40	69	18.0	195	10	Q94CL9
41	68.5	17.9	209	10	Q9SCR2
42	67.5	17.6	246	3	Q03973
43	67	17.5	160	8	Q47326
44	67	17.5	882	11	Q9R081
45	67	17.5	910	11	Q922L5

ALIGNMENTS

RESULT 1

Q43806	PRELIMINARY;	PRT;	158 AA.
AC	Q43806;		
DT	01-JUN-1998 (TREMBLrel. 06, Created)		
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	P27 kipl protein (Fragment).		
GN	P27 KIPL.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID:9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=BREAST CARCINOMA,		
EX	MEDLINE=96140757; PubMed=8557259;		
RA	Ferrando A A, Balbin M, Pendas A M, Vizoso F, Velasco G.,		
RA	Lopez-Otin C.		
RT	"Mutational analysis of the human cyclin-dependent kinase inhibitor		
RT	P27 kipl in primary breast carcinomas."		
RI	Hom Genet. 97:91-94(1996).		
DR	EMBL; X84849; CAA59284.1; .		
DR	InterPro: IPR003175; CDI.		
DE	Pfam: PF02334, CDI, 1.		
FT	VARIANT 109, 109 G -> V.		
FT	NON_TER 158 158		
SQ	SEQUENCE 158 AA: 17651 MW; LB622905BA2FD150 CRC64;		

Query Match	100.0%	Score	645, [6.4, Length 158;
Best Local Similarity	100.0%	Pred. No. 1.1e-34;	
Matches	67, Conservative	0; Mismatches	0; Indels 0; Gaps 0;
QY	1	EHPKPSACENFGVVDHLLFMLEKHCQPMEEASQRKWNFDQNHKPLEGKYEQVEVK	60
ddb	22	EHPKPSACENFGVVDHLLFMLEKHCQPMEEASQRKWNFDQNHKPLEGKYEQVEVK	81
QY	61	GSLPETY 67	


```
QY 1 EHPKPSACRNLFQGVDPVHEELTRDLEKHCRCRMEASQPKWNFDONHKPLEGKYEWQVEVK 60
DB 14 EYPKPSACRNLFQGVDPVHEELTRDLEKHCRCRMEASQPKWNFDONHKPLEGKYEWQVEVK 73
QY 61 GSLPEFY 67
DB 74 GSLPEFY 80

RESULT 6
Q08769
ID Q08769 PPBLIMINARY: PPT: 197 AA.
AC Q08769;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE P27 Kipl.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Patus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawada M., Yamagoe S., Uehara Y.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kawada M., Yamagoe S., Kazuo S., Mizuno S., Uehara Y.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Kawada M., Yamagoe S., Murakami Y., Suzuki K., Mizuno S., Uehara Y.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA STRAIN-SPRAGUE-DAWLEY;
RC Dastvan F., Reidy M.A.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: D86424; BAA19960.1;
DR EMBL: AF015194; AAB71368.1;
DR InterPro: IPR003175, GCI.
DR Pfam: PF02234; CDI: 1.
SQ SEQUENCE 197 AA; 22139 MW; 55738078274847F CPG64;

Query Match: 97.1%; Score 372; DB 11; Length 197;
Best Local Similarity 95.5%; Pred. No. 2.3e-33;
Matches 64; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACRNLFQGVDPVHEELTRDLEKHCRCRMEASQPKWNFDONHKPLEGKYEWQVEVK 60
DB 22 EHPKPSACRNLFQGVDPVHEELTRDLEKHCRCRMEASQPKWNFDONHKPLEGKYEWQVEVK 81
QY 61 GSLPEFY 67
DB 82 GSLPEFY 88

RESULT 7
Q035792
ID Q035792 PPBLIMINARY: PPT: 197 AA.
AC Q035792;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE P27.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Patus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-SPRAGUE-DAWLEY;
RC Tissue-Spleen;
RL MEDLINE=97361761; PubMed=9218722;
RX
```

```
PA Nomura H., Sawada Y., Fujinaga K., Ohtaki S.;
RT *Cloning and characterization of rat p27Kipl, a cyclin-dependent
RT kinase inhibitor.;
RL Gene 191-218(1997);
DR EMBL: D83792; BAA21561.1;
DR InterPro: IPR003175; CDI: 1.
DR Pfam: PF02234; CDI: 1.
SQ SEQUENCE 197 AA; 22112 MW; 55738078274847F CPG64;

Query Match: 97.1%; Score 372; DB 11; Length 197;
Best Local Similarity 95.5%; Pred. No. 2.3e-33;
Matches 64; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACRNLFQGVDPVHEELTRDLEKHCRCRMEASQPKWNFDONHKPLEGKYEWQVEVK 60
DB 22 EHPKPSACRNLFQGVDPVHEELTRDLEKHCRCRMEASQPKWNFDONHKPLEGKYEWQVEVK 81
QY 61 GSLPEFY 67
DB 82 GSLPEFY 88

RESULT 8
Q09BDC3
ID Q09BDC3 PPBLIMINARY: PPT: 198 AA.
AC Q09BDC3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE P27Kipl.
GN P27Kipl.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Hirano K., Hirano M., Zeng Y., Nishimura J., Hara K., Muta K.;
RA Nawata H., Kanaike H.;
RT *Cloning and functional expression of a degradation-resistant novel
RT isoform of p27Kipl.;
RL Biochem. Biophys. Res. Commun. 257:1-57(2001)
DR EMBL: AB031957; BAB39727.1;
DR EMBL: AB031355; BAB39725.1;
DR EMBL: AF015194; AAB71368.1;
DR InterPro: IPR003175; CDI: 1.
DR Pfam: PF02234; CDI: 1.
SQ SEQUENCE 198 AA; 22201 MW; E5B01D225E5BDD5F CPG64;

Query Match: 97.1%; Score 372; DB 6; Length 198;
Best Local Similarity 97.0%; Pred. No. 2.3e-33;
Matches 65; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EHPKPSACRNLFQGVDPVHEELTRDLEKHCRCRMEASQPKWNFDONHKPLEGKYEWQVEVK 60
DB 22 EHPKPSACRNLFQGVDPVHEELTRDLEKHCRCRMEASQPKWNFDONHKPLEGKYEWQVEVK 81
QY 61 GSLPEFY 67
DB 82 GSLPEFY 88

RESULT 9
Q09YX4
ID Q09YX4 PPBLIMINARY: PPT: 179 AA.
AC Q09YX4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE P27-like cyclin-dependent kinase inhibitor.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```



```

[4]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; TISSUE=BREAST TUMOR;
RA Strausberg K.;
DR EMBL: AJ276595; CAC16482.1;
DR EMBL: AF160190; AAF06943.1;
DR EMBL: BC005412; AAF05412.1;
DR MGD: MGI:104564; Cdkn1c;
DR InterPro: IPR003175; CDI;
DR Pfam: PF02234; CDI; 1;
KW Kinase.
SQ SEQUENCE 335 AA; 35903 MW; 65C40675287F84F CRC64;

Query Match 45.4%; Score 174; DB 11; Length 335;
Best Local Similarity 47.0%; Pred. No. 2.8e-11;
Matches 31; Conservative 12; Mismatches 27; Indels 2; Gaps 1;

QY 4 KPSACPNLFGPVDRHEELIRDLKKHKCKMEEASQPKWNFDQNHKPLE--GKYEWQVEKGS b1
DQ : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 15 RSSACKSLFGPVDRHEELGKELMKLAELNADLNKWNDFNQDVLKPGKGLWNEVDSE 74
DQ : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 62 SLPFY 67
DQ 75 SVPAFY 80
DQ 164 AA.

RESULT 13
QY 64415 PRELIMINARY; PRT: 164 AA.
AC 64415;
DI 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE P21 (WAF1).
GN WAF1 OR CIP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Belinsky S.A.;
RX MEDLINE=95316868; PubMed=7796420;
RA el-Deiry W.S., Tokino T., Waldman T., Velculescu V., Oliner J.D.,
RA Hurrell M., Hill D.E., Rees J.L., Hamilton S.R., Kinzler K.W.,
RA Vogelstein B.;
RT "Topological control of p21WAF1/CIP1 expression in normal and
RT neoplastic tissues."
RL Cancer Res. 55:2910-2919(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=F344/N; TISSUE=LUNG;
RA Belinsky S.A.;
RL Submitted (09-1995) to the EMBL/GenBank/TrEMBL databases
DR EMBL: U24174; AAC52221.1;
DR EMBL: U41275; AAC42084.1;
DR InterPro: IPR003175; CDI;
DR Pfam: PF02234; CDI; 1;
SQ SEQUENCE 164 AA; 18318 MW; 6057E86045B6435F CRC64;

Query Match 41.8%; Score 160; DB 11; Length 164;
Best Local Similarity 42.2%; Pred. No. 4.4e-10;
Matches 27; Conservative 10; Mismatches 27; Indels 0; Gaps 0.

QY 4 KPSACPNLFGPVDRHEELIRDLKKHKCKMEEASQPKWNFDQNHKPLE--GKYEWQVEKGS b3
DQ : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 13 RSSACKSLFGPVDRHEELGKELMKLAELNADLNKWNDFNQDVLKPGKGLWNEVDSE 72
DQ : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 64 PFY 67
DQ 73 PKY 76
```

```

RESULT 14
QY 96LE1 PRELIMINARY; PRT: 164 AA.
AC 96LE1;
DI 01-DEC-2001 (TrEMBLrel. 14, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cyclin-dependent kinase inhibitor isoform.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li L.-C., Zhao H., Dahiya R.;
KL "Cloning and Characterization of p21 Isoform."
RL Submitted (Sep-2000) to the EMBL/GenBank/TrEMBL databases.
DR EMBL: AY008263; AAG15411.1;
DR InterPro: IPR003175; CDI;
DR Pfam: PF02234; CDI; 1;
KW Kinase.
SQ SEQUENCE 164 AA; 17827 MW; 378B002161F83B07 CRC64;

Query Match 39.9%; Score 153; DB 4; Length 164;
Best Local Similarity 44.3%; Pred. No. 2.6e-09;
Matches 27; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY 7 ACNPLFGPVDRHEELIRDLKKHKCKMEEASQPKWNFDQNHKPLE--GKYEWQVEKGS b6
DQ : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 17 ACNPLFGPVDRHEELIRDLKKHKCKMEEASQPKWNFDQNHKPLE--GKYEWQVEKGS b6
DQ : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 67 Y 67
DQ 77 Y 77

RESULT 15
QY 14313 PRELIMINARY; PRT: 181 AA.
AC 14313;
DI 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cyclin-dependent kinase (fragment).
GN CIP1/WAF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TUMOR;
RX MEDLINE=95384154; PubMed=7655464;
PA Mosses S., Gehl H., Lee P.D., Malkin D., Bull S.R., Andriulis I.L.;
RT "Two variants of the CIP1/WAF1 gene occur together and are associated
RT with human cancer."
PL Hum. Mol. Genet. 4:1089-1092(1995)
DR EMBL: L47332; AAB59559.1;
DR InterPro: IPR003175; CDI;
DR Pfam: PF02234; CDI; 1;
KW Kinase.
RN [2]
RP SEQUENCE 181 AA; 25083 MW; 4CCFA5112332D4F1 CRC64;

Query Match 39.4%; Score 151; DB 4; Length 181;
Best Local Similarity 44.3%; Pred. No. 4.8e-09;
Matches 27; Conservative 9; Mismatches 25; Indels 0; Gaps 0;

QY 7 ACNPLFGPVDRHEELIRDLKKHKCKMEEASQPKWNFDQNHKPLE--GKYEWQVEKGS b6
DQ : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 34 ACNPLFGPVDRHEELIRDLKKHKCKMEEASQPKWNFDQNHKPLE--GKYEWQVEKGS b6
DQ : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 67 Y 67
```

11 01 Y 04

Generated by mpf (rspt) on: May 30, 2003, 09:01:29
File Name: 186006.saves

XX 06-AUG-1998.
 PD 03-FEB-1998; 98WO-US01893.
 PF 03-FEB-1997; 97US-0794002.
 PR (HUTG-) HITCHINSON CANCER RES CENT FRED.
 PA Porter PL, Roberts JM.
 PI WPI: 1998-437612/37.
 DR N-PSDB; AAY47518.
 XX Assays for protein p27 inhibiting activation of cyclin E-Cdk2
 PT complex - useful for, e.g. diagnosis and prognosis of cancer,
 PT especially breast carcinoma
 PS Disclosure: Fig 14B; 105pp; English.
 CC The present sequence represents a 27 kDa protein (p27 or Kip1) which
 CC inhibits the activation of a cyclin E-cyclin-dependent kinase2 (Cdk2)
 CC complex. A reduced relative level of kip1 is indicative of a
 CC hyperproliferative disease (particularly cancer, especially breast
 CC carcinoma) and also is prognostic for increased risk of death and/or
 CC recurrence of cancer (and may be used to determine suitable treatments).
 CC Agents that affect the activity of kip1 can be used to treat
 CC hyperproliferative conditions, e.g. to stimulate tissue or organ repair
 CC or to establish cell cultures.
 CC
 XX Sequence 197 AA:
 SO
 Query Match 100.0%; Score 1051; DB 19; Length 197;
 Best Local Similarity 100.0%; Pred No. 1 le-101;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSNVRVNSGSPSLERMDARQADHPKPSACRNLEGPVNHBELTRDEKHCROMEASORKW 60
 Db 1 MSNVRVNSGSPSLERMDARQADHPKPSACRNLEGPVNHBELTRDEKHCROMEASORKW 60
 QY 61 NDFQGNHKKLEGRYEMQEVYRGSLEFFYKPKPKPSACKVLAQESQVVSRRQAVPLIG 120
 Db 61 NDFQGNHKKLEGRYEMQEVYRGSLEFFYKPKPKPSACKVLAQESQVVSRRQAVPLIG 120
 QY 121 SQANSEDRHLVDQMPSSDNDAGIAFCPPGMKPPAAPPSSQNKFPANPTEENVSDSPN 180
 Db 121 SQANSEDRHLVDQMPSSDNDAGIAFCPPGMKPPAAPPSSQNKFPANPTEENVSDSPN 180
 QY 181 AGIVEQTPKKPKGLRRQT 197
 Db 181 AGIVEQTPKKPKGLRRQT 197
 RESULT 4
 AAY08819
 ID AAY08819 standard; Protein: 197 AA.
 AC AAY08819;
 XX
 DT 13-AUG-1999 (first entry)
 XX
 DE Mouse wild type p27 protein.
 XX
 KW Activation sequence; transcription factor; murine; p163; p27; treatment;
 KW binding protein; DNA binding domain; effector gene; disease; infection;
 KW tumour; leukaemia; autoimmune disease; allergy; arthritis; inflammation;
 KW transplant rejection; graft-versus host disease; circulatory disorder;
 KW blood clot; anaemia; hormonal disorder; CNS injury.
 XX
 OS Mus sp.
 XX EP926237-A2.
 XX PN

PD 30-JUN-1999.
 XX
 XX 12-DEC-1998; 98EP-0123709.
 XX
 XX 20-DEC-1997; 97DE-1056975.
 PR (HMBI) HOFMIST MARION ROUSSEL DEUT GMBH.
 PA Buerger A, Eilers M, Sedlacek H.
 PI WPI: 1999-349238/30.
 DR
 XX
 XX New nucleic acid construct comprising promoter, transcription factor
 PT gene, activation sequence and effector gene - useful for gene
 PT therapy treatment of allergies, inflammation, transplant disorders
 PT and leukaemia
 PS Disclosure: Page 49; 90pp; German.
 CC This invention describes a novel nucleic acid construct comprising the
 CC following components (a) an activation sequence for the transcription
 CC of component b, (b) component b which is constructed from component b1
 CC (a transcription factor activating domain), component b2 (murine p163
 CC or p27 binding protein) and component b3 (a transcription factor DNA
 CC binding domain); (c) an activation sequence which is activated by binding
 CC of the expression product of component (b) and which induces
 CC transcription of component (d) and (d) an effector gene. The construct,
 CC preferably in a plasmid or viral vector, or cell can be used to treat a
 CC disease selected from infections, tumours, leukaemia, autoimmune
 CC diseases, allergies, arthritis, inflammations, transplant rejection,
 CC graft-versus host disease, blood clotting disorders, circulatory
 CC disorders, anaemia, hormonal disorders and CNS injuries. This sequence
 CC represents the murine p27 protein which is used in the method of the
 CC invention.
 CC
 XX Sequence 197 AA:
 SO
 Query Match 100.0%; Score 1051; DB 20; Length 197;
 Best Local Similarity 100.0%; Pred No. 1 le-101;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSNVRVNSGSPSLERMDARQADHPKPSACRNLEGPVNHBELTRDEKHCROMEASORKW 60
 Db 1 MSNVRVNSGSPSLERMDARQADHPKPSACRNLEGPVNHBELTRDEKHCROMEASORKW 60
 QY 61 NDFQGNHKKLEGRYEMQEVYRGSLEFFYKPKPKPSACKVLAQESQVVSRRQAVPLIG 120
 Db 61 NDFQGNHKKLEGRYEMQEVYRGSLEFFYKPKPKPSACKVLAQESQVVSRRQAVPLIG 120
 QY 121 SQANSEDRHLVDQMPSSDNDAGIAFCPPGMKPPAAPPSSQNKFPANPTEENVSDSPN 180
 Db 121 SQANSEDRHLVDQMPSSDNDAGIAFCPPGMKPPAAPPSSQNKFPANPTEENVSDSPN 180
 QY 181 AGIVEQTPKKPKGLRRQT 197
 Db 181 AGIVEQTPKKPKGLRRQT 197
 RESULT 5
 AAY08847
 ID AAY08847 standard; Protein: 197 AA.
 AC AAY08847;
 XX
 DT 13-AUG-1999 (first entry)
 XX
 DE Murine wild type p27 protein.
 XX
 KW p163; murine; p27 inhibitor; p27-induced inhibition; cell proliferation;
 KW p27 binding domain; Ran binding domain; detection; screening; malignancy;
 KW tumour; mutant; p27 protein.
 XX
 OS Mus sp.

DB 121 SCANSIDRLVDQMPDSSDNGALAGCGMKRPAEDSSSNKRANKTEENVSDDSPN 180
 QY 181 ACTVEOTPKKPGRLRRQT 197
 DB 181 ACTVEOTPKKPGRLRRQT 197

RESULT 7
 AAY08811
 ID AAY08811 standard; Protein; 212 AA.
 AC AAY08811;
 XX
 DT 13-AUG-1999 (first entry)
 DE Mouse p27 protein consensus sequence.
 XX
 KW Activation sequence; transcription factor; murine; p163; p27; treatment;
 KW binding protein; DNA binding domain; effector gene; disease; infection;
 KW tumour; leukaemia; autoimmune disease; allergy; arthritis; inflammation;
 KW transplant rejection; graft-versus-host disease; circulatory disorder;
 KW blood clot; anaemia; hormonal disorder; CNS injury.
 XX
 OS Mus sp.
 PN EP926237-A2.
 XX
 PD 30-JUN-1999.
 XX
 PF 12-DEC-1998; 98EP-0123709.
 XX
 PR 20-DEC-1997; 97DE-1056975.
 XX
 PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.
 PI Buerquin A, Eilers M, Sedlacek H;
 DR WPI; 1999-349237/30.
 XX
 PT New nucleic acid construct comprising promoter, transcription factor
 PT gene, activation sequence and effector gene - useful for gene
 PT therapy treatment of allergies, inflammation, transplant disorders
 PT and leukaemia
 XX
 PS Disclosure: Page 49; 90pp; German.
 XX
 CC This invention describes a novel nucleic acid construct comprising the
 CC following components (a) an activation sequence for the transcription
 CC of component b, (b) component b which is constructed from component b1
 CC (a transcription factor activating domain), component b2 (murine p163
 CC or p27 binding protein) and component b3 (a transcription factor DNA
 CC binding domain), (c) an activation sequence which is activated by binding
 CC of the expression product of component (b) and which induces
 CC transcription of component (d) and (d) an effector gene. The construct,
 CC preferably in a plasmid or viral vector, or cell can be used to treat a
 CC disease selected from infections, tumours, leukaemia, autoimmune
 CC diseases, allergies, arthritis, inflammations, transplant rejection,
 CC graft-versus-host disease, blood clotting disorders, circulatory
 CC disorders, anaemia, hormonal disorders and CNS injuries. This sequence
 CC represents the murine p27 protein consensus sequence which is used to
 CC describe the method of the invention.
 XX
 SQ Sequence 212 AA:
 Query Match 96.7% Score 1016; RA 20; Length 212;
 Best Local Similarity 99.0%; Pred No. 5,4e-98;
 Matches 191, Conservative 0; Mismatches 2; Indels 0; Gaps 0.

OY 5 RVSNQSPSLFPMADARQADHPKPSAATPNI.FPYNHELTPLFKHPQMEASQPKWNPDP A4
 DB 1 RVSNQSPSLFPMADARQADHPKPSAATPNI.FPYNHELTPLFKHPQMEASQPKWNPDP bu

OY 65 QNKRPLDQKYFWQVPEKSSLPLEFYKPKPKKSAKYLAEFSQVSSQKAVPLTSSQAN 124
 DB 61 QNKRPLDQKYFWQVPEKSSLPLEFYKPKPKKSAKYLAEFSQVSSQKAVPLTSSQAN 120
 OY 125 SEDRLVDQMPDSSDNGALAGCGMKRPAEDSSSNKRANKTEENVSDDSPN 184
 DB 121 SEDRLVDQMPDSSDNGALAGCGMKRPAEDSSSNKRANKTEENVSDDSPN 180
 OY 185 EQTPKPKPGRLRRQT 197
 DB 181 EQTPKPKPGRLRRQT 193

RESULT 8
 AAY08839
 ID AAY08839 standard; Protein; 212 AA.
 AC AAY08839;
 XX
 DT 13-AUG-1999 (first entry)
 DE Murine p27 protein consensus sequence.
 XX
 KW p163; murine; p27 inhibitor; p27-induced inhibition; cell proliferation;
 KW p27 binding domain; Ran binding domain; detection; screening; malignancy;
 KW tumour; p27 protein.
 XX
 OS Mus sp.
 PN EP926236-A1.
 XX
 PD 30-JUN-1999.
 XX
 PF 12-DEC-1998; 98EP-0123708.
 XX
 PR 20-DEC-1997; 97DE-1056975.
 XX
 PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.
 PI Buerquin A, Eilers M, Sedlacek H;
 DR WPI; 1999-349237/30.
 XX
 PT New p27-inhibiting protein p163 and DNA - useful for detection
 PT and/or quantification of p163 mRNA
 XX
 PS Disclosure: Page 28; 68pp; German.
 XX
 CC This invention describes (1) a protein that inhibits p27 and thereby
 CC arrests p27-induced inhibition of cell proliferation, (2) the protein of
 CC (1) comprising at least part of the amino acid sequence of murine p163,
 CC (3) a protein that can be derived from the protein of (2) by deletion of
 CC the p27 binding domain or the Ran binding domain, (4) a protein that can
 CC be derived from the protein of (2) by deletion of all amino acid
 CC sequences other than the p27 binding domain, (5) a protein that is the
 CC human or other mammalian species homologue of a protein as in (1)-(4),
 CC (6) DNA encoding the p163 protein, (7) antibodies and antibody fragments
 CC that bind to the p27 binding domain of a protein as above, (8) antibodies
 CC and antibody fragments that bind to the Ran binding domain of a protein
 CC as above, (9) antisense nucleic acids complementary to portions of the
 CC DNA of (6) between codons 121 and 467, (10) a nucleic acid construct
 CC coding for an antisense nucleic acid as in (9) for inhibiting the
 CC proliferation of a cell, in which DNA coding for the antisense nucleic
 CC acid sequence is linked to at least one activation sequence and is
 CC introduced into the target cell as naked DNA or as an insert in a
 CC vector, and (11) a nucleic acid construct containing the
 CC DNA of (6) linked to an activation sequence that permits expression of a
 CC protein as above in a cell. The DNA of (6) can be used for detection
 CC and/or quantification of p163 mRNA in cells and/or tissues, preferably by
 CC Northern blotting, PCR or fluorescent in situ hybridization. The proteins
 CC can be used to produce antibodies, which can be used to detect the
 CC corresponding protein in cells, tissues or body fluids. The antisense
 CC nucleic acids can be used to inhibit cell proliferation in vitro or in

CC This invention describes (1) a protein that inhibits p27 and thereby
 CC arrests p27-induced inhibition of cell proliferation, (2) the protein of
 CC (1) comprising at least part of the amino acid sequence of murine p163,
 CC (3) a protein that can be derived from the protein of (2) by deletion of
 CC the p27 binding domain or the p27 binding domain, (4) a protein that can
 CC be derived from the protein of (2) by deletion of all amino acid
 CC sequences other than the p27 binding domain, (5) a protein that is the
 CC human or other mammalian species homologue of a protein as in (1)-(4),
 CC (6) DNA encoding the p163 protein, (7) antibodies and antibody fragments
 CC that bind to the p27 binding domain of a protein as above, (8) antibodies
 CC and antibody fragments that bind to the p27 binding domain of a protein
 CC as above, (9) antisense nucleic acids complementary to portions of the
 CC DNA of (6) between codons 121 and 467, (10) a nucleic acid construct
 CC coding for an antisense nucleic acid as in (9) for inhibiting the
 CC proliferation of a cell, in which DNA coding for the antisense nucleic
 CC acid sequence is linked to at least one activation sequence and is
 CC introduced into the target cell as naked DNA or as an insert in a
 CC nonviral or viral vector and (11) a nucleic acid construct containing the
 CC DNA of (6) linked to an activation sequence that permits expression of a
 CC protein as above in a cell. The DNA of (6) can be used for detection of a
 CC and/or quantification of p163 mRNA in cells and/or tissues, preferably by
 CC Northern blotting, PCR or fluorescent in-situ hybridisation. The proteins
 CC can be used to produce antibodies, which can be used to detect the
 CC corresponding protein in cells, tissues or body fluids. The antisense
 CC nucleic acids can be used to inhibit cell proliferation in vitro or in
 CC vivo. The proteins can be used to screen for substances that inhibit the
 CC interaction between the proteins and their cellular binding partners,
 CC preferably using a two hybrid system or using an affinity system in which
 CC p163 or its p27-binding domain is immobilised on a solid phase, the solid
 CC phase is incubated with a test substance, and the inhibition of the
 CC binding of a labelled binding partner of p163 (especially p27 or p40) is
 CC measured. Assays for p163 can be used to assess the malignancy of
 CC tumours. This sequence represents a mutant mouse p27 protein sequence
 CC isolated from clone #294 which is used to describe the method of the
 CC invention.

CC Sequence 199 AA:

Query Match 95.6%, Score 1005, DB 20, Length 199;
 Best Local Similarity 97.9%; Pred. No. 7a-97;
 Matches 189; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 RVNSGSPSLERMDARQADHPKPSACRNLFQPVNHELTDLKHCROMEASQKWNEDF 64
 DB 1 RVNSGSPSLERMDARQADHPKPSACRNLFQPVNHELTDLKHCROMEASQKWNEDF 60
 QY 65 QNHKLEBRYEMQEVKESLPFEFYKPPPKPSACKVLAQSSQVSSQKAVPLIGSAN 124
 DB 61 QNHKLEBRYEMQEVKESLPFEFYKPPPKPSACKVLAQSSQVSSQKAVPLIGSAN 120
 QY 125 SEDRLVDQMPGSSNAGLAAGCPGMKKKPAAEIASSQNKANPIEENVSDGSPNAGTV 184
 DB 121 SEDRLVDQMPGSSNAGLAAGCPGMKKKPAAEIASSQNKANPIEENVSDGSPNAGTV 180
 QY 185 QTPKKPGCLRQOT 197
 DB 181 QTPKKPGCLRQOT 193

RESULT 11

AAV08815 standard; Protein: 199 AA.

AAV08815;

13-AUG-1999 (first entry)

Mouse p27 mutant protein 4.

Activation sequence; transcription factor, murine; p163; p27; treatment;
 binding protein; DNA binding domain, effector gene, disease, infection;
 tumour, leukaemia, autoimmune disease, allergy, arthritis, inflammatory;
 transplant rejection, graft-versus-host disease, circulatory disorder.

KW blood clot; anaemia; hormonal disorder; CNS injury; mutant.
 XX Mus sp.
 OS EPR2F237-A2
 PN 30-JUN-1999.
 XX 12-DEC-1998; 98EP 0123709.
 XX 20-DEC-1997; 97EP-1056975.
 XX (EMRI) HOECHST MARION ROUSSEL, DEUT GMBH.
 PA Bueglin A, Eilers M, Sedlacek H;
 PI WPL; 1999-349238/30.

PT New nucleic acid construct comprising promoter, transcription factor
 PT gene, activation sequence and effector gene - useful for gene
 PT therapy, treatment of allergies, inflammation, transplant disorders
 PT and leukaemia

PS Disclosure, Page 49, 50pp; German.

CC This invention describes a novel nucleic acid construct comprising the
 CC following components (a) an activation sequence for the transcription
 CC of component b, (b) component b which is constructed from component b1
 CC (a transcription factor activating domain), component b2 (murine p163
 CC or p27 binding protein) and component b3 (a transcription factor DNA
 CC binding domain); (c) an activation sequence which is activated by binding
 CC of the expression product of component (b) and which induces
 CC transcription of component (d) and (d) an effector gene. The construct,
 CC preferably in a plasmid or viral vector, can be used to treat a
 CC disease selected from infections, tumours, leukaemia, autoimmune
 CC diseases, allergies, arthritis, inflammations, transplant rejection,
 CC graft-versus-host disease, blood clotting disorders, circulatory
 CC disorders, anaemia, hormonal disorders and CNS injuries. This sequence
 CC represents a mutant murine p27 protein which is used to describe the
 CC method of the invention

CC Sequence 199 AA:

Query Match 95.5%, Score 1004, DB 20, Length 199;
 Best Local Similarity 98.4%; Pred. No. 8, 9a-97;
 Matches 189; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 VNSGSPSLERMDARQADHPKPSACRNLFQPVNHELTDLKHCROMEASQKWNEDF 65
 DB 1 VNSGSPSLERMDARQADHPKPSACRNLFQPVNHELTDLKHCROMEASQKWNEDF 60
 QY 66 QNHKLEBRYEMQEVKESLPFEFYKPPPKPSACKVLAQSSQVSSQKAVPLIGSAN 125
 DB 61 QNHKLEBRYEMQEVKESLPFEFYKPPPKPSACKVLAQSSQVSSQKAVPLIGSAN 120
 QY 126 SEDRLVDQMPGSSNAGLAAGCPGMKKKPAAEIASSQNKANPIEENVSDGSPNAGTV 185
 DB 121 SEDRLVDQMPGSSNAGLAAGCPGMKKKPAAEIASSQNKANPIEENVSDGSPNAGTV 180
 QY 186 QTPKKPGCLRQOT 197
 DB 181 QTPKKPGCLRQOT 192

RESULT 12

AAV08843 standard; Protein: 199 AA.

AAV08843;

13-AUG-1999 (first entry)

Murine mutant p27 protein from clone #660.

QY 3 NVKVSNSGSLERMAAPKAPKPSA*PNIKPVNHEITPLEKRTMTMEASPKWNF 62
 DB 1 NVKVSNSGSLERMAAPKAPKPSA*PNIKPVNHEITPLEKRTMTMEASPKWNF 59
 QY 63 PFGNKRPLEGPEYFMEQVEFEGSLPEFYPPPPPKSACVVLQESQADVCSQAVPLISQ 122
 DB 60 PFGNKRPLEGPEYFMEQVEFEGSLPEFYPPPPPKSACVVLQESQADVCSQAVPLISQ 119
 QY 123 ANSEDRHLVDQMPDSSNQAGLAFQCPGMKPPAAEFSSQSNKPANRTEENVSDGSPNAG 182
 DB 120 ANSEDRHLVDQMPDSSNQAGLAFQCPGMKPPAAEFSSQSNKPANRTEENVSDGSPNAG 179
 QY 183 TVEQTPKKPKGLRROT 197
 DB 180 TVEQTPKKPKGLRROT 194

RESULT 14
 AAY08844
 ID AAY08844 standard; Protein; 220 AA.
 XX
 AC AAY08844;
 DT 13-AUG-1999 (first entry)
 XX
 DE Murine mutant p27 protein from clone #687
 XX
 KM p163; murine; p27 inhibitor; p27-induced inhibition; cell proliferation;
 KM p27 binding domain; Ran binding domain; detection; screening; malignancy;
 KM tumour; mutant; p27 protein.
 XX
 OS Mus sp.
 PN EP926236.A1.
 PD 30-JUN-1999.
 PF 12-DEC-1998; 98BP-0123708.
 PR 20-DEC-1997; 97DE-1056975.
 XX
 PA (HMR1) HOECHST MARTON ROUSSEL DEUT GMBH.
 PI Buerquin A, Eilers M, Sedlacek H;
 DR WPI: 1999-349237/30.
 XX
 PT New p27-inhibiting protein p163 and DNA - useful for detection
 PT and/or quantification of p163 mRNA
 PS Disclosure: Page 28; 68pp; German.
 XX
 CC This invention describes (1) a protein that inhibits p27 and thereby
 CC arrests p27-induced inhibition of cell proliferation, (2) the protein of
 CC (1) comprising at least part of the amino acid sequence of murine p163,
 CC (3) a protein that can be derived from the protein of (2) by deletion of
 CC the p27 binding domain or the Ran binding domain, (4) a protein that can
 CC be derived from the protein of (2) by deletion of all amino acid
 CC sequences other than the p27 binding domain, (5) a protein that is the
 CC human or other mammalian species homologue of a protein as in (1)-(4),
 CC (6) DNA encoding the p163 protein, (7) antibodies and antibody fragments
 CC that bind to the p27 binding domain of a protein as above, (8) antibodies
 CC and antibody fragments that bind to the Ran binding domain of a protein
 CC as above, (9) antisense nucleic acids complementary to portions of the
 CC DNA of (6) between codons 121 and 467, (10) a nucleic acid construct
 CC coding for an antisense nucleic acid as in (9) for inhibiting the
 CC proliferation of a cell, in which DNA coding for the antisense nucleic
 CC acid sequence is linked to at least one activation sequence and is
 CC introduced into the target cell as naked DNA or as an insert in a
 CC nonviral or viral vector and (11) a nucleic acid construct containing the
 CC DNA of (6) linked to an activation sequence that permits expression of a
 CC protein as above in a cell. The DNA of (6) can be used for detection
 CC and/or quantification of p163 mRNA in cells and/or tissues, preferably by

CC Northern blotting, PCR or fluorescent in-situ hybridisation. The proteins
 CC can be used to produce antibodies, which can be used to detect the
 CC corresponding protein in cells, tissues or body fluids. The antisense
 CC nucleic acids can be used to inhibit cell proliferation in vitro or in
 CC vivo. The proteins can be used to screen for substances that inhibit the
 CC interaction between the proteins and their cellular binding partners,
 CC preferably using a two hybrid system or using an affinity system in which
 CC p163 or its p27-binding domain is immobilised on a solid phase, the solid
 CC phase is incubated with a test substance, and the inhibition of the
 CC binding of a labelled binding partner of p163 (especially p27 or Ran) is
 CC measured. Assays for p163 can be used to assess the malignancy of
 CC tumours. This sequence represents a mutant mouse p27 protein sequence
 CC isolated from clone #687 which is used to describe the method of the
 CC invention.
 CC
 XX Sequence 220 AA;
 SO
 S0

Query Match 95.5%; Score 1003.5; DR 20; Length 220;
 Best Local Similarity 97.9%; Pred. No. 1.2e-96;
 Matches 191; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3 NVKVSNSGSLERMAAPKAPKPSA*PNIKPVNHEITPLEKRTMTMEASPKWNF 62
 DB 1 NVKVSNSGSLERMAAPKAPKPSA*PNIKPVNHEITPLEKRTMTMEASPKWNF 59
 QY 63 PFGNKRPLEGPEYFMEQVEFEGSLPEFYPPPPPKSACVVLQESQADVCSQAVPLISQ 122
 DB 60 PFGNKRPLEGPEYFMEQVEFEGSLPEFYPPPPPKSACVVLQESQADVCSQAVPLISQ 119
 QY 123 ANSEDRHLVDQMPDSSNQAGLAFQCPGMKPPAAEFSSQSNKPANRTEENVSDGSPNAG 182
 DB 120 ANSEDRHLVDQMPDSSNQAGLAFQCPGMKPPAAEFSSQSNKPANRTEENVSDGSPNAG 179
 QY 183 TVEQTPKKPKGLRROT 197
 DB 180 TVEQTPKKPKGLRROT 194

RESULT 15
 AAY08813
 ID AAY08813 standard; Protein; 199 AA.
 XX
 AC AAY08813;
 DT 13-AUG-1999 (first entry)
 XX
 DE Mouse p27 mutant protein 2.
 XX
 KM Activation sequence; transcription factor; murine; p163; p27; treatment;
 KM binding protein; DNA binding domain; effector gene; disease; infection;
 KM tumour; leukemia; autoimmune disease; allergy; arthritis; inflammation;
 KM transplant rejection; graft versus host disease; circulatory disorder;
 KM blood clot; anaemia; hormonal disorder; CNS injury; mutant.
 XX
 OS Mus sp.
 PN EP926237.A1.
 PD 30-JUN-1999.
 PF 12-DEC-1998; 98BP-0123709.
 PR 20-DEC-1997; 97DE-1056975.
 XX
 PA (HMR1) HOECHST MARTON ROUSSEL DEUT GMBH.
 PI Buerquin A, Eilers M, Sedlacek H;
 DR WPI: 1999-349238/30.
 XX
 PT New nucleic acid construct comprising promoter, transcription factor
 PT gene, activation sequence and effector gene - useful for gene
 PT therapy treatment of allergies, inflammation, transplant disorders

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 08:55:37 Search time: 14.7621 seconds
(without alignments)
392.644 Million cell updates/sec

Title: US-09-865-018B-4

Perfect score: 1051
Sequence: 1 MSNVRVSNMSEFLEMDAKQ...SPNATVHQLTKKPIIKPKYI 197

Scoring table: R10SUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

Issued_Patents_AA:
1: /cgn2_6/ptodata/1/aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/1/aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/aa/PT05.COMB.pep:*
6: /cgn2_6/ptodata/1/aa/backfiles1.pep.*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1051	100.0	197	US-08-275-983B-2	Sequence 2, Appli
2	1051	100.0	197	US-09-240-906-8	Sequence 8, Appli
3	1051	100.0	197	US-09-215-221-57	Sequence 57, Appli
4	1051	100.0	197	US-08-794-002-4	Sequence 4, Appli
5	1042	99.1	197	US-08-854-039B-4	Sequence 4, Appli
6	1040	99.0	197	US-08-415-655-6	Sequence 6, Appli
7	1016	96.7	212	US-09-215-221-49	Sequence 19, Appli
8	1005	95.5	194	US-09-215-221-52	Sequence 52, Appli
9	1004	95.5	193	US-09-215-221-53	Sequence 53, Appli
10	1003.5	95.5	195	US-09-215-221-54	Sequence 54, Appli
11	994	94.6	194	US-09-215-221-55	Sequence 55, Appli
12	948	90.2	180	US-09-215-221-55	Sequence 55, Appli
13	944	89.8	180	US-09-215-221-50	Sequence 50, Appli
14	931	88.6	198	US-08-406-248-4	Sequence 4, Appli
15	931	88.6	198	US-08-897-333A-2	Sequence 2, Appli
16	931	88.6	198	US-09-240-906-6	Sequence 6, Appli
17	931	88.6	198	US-08-794-002-2	Sequence 2, Appli
18	931	88.6	198	US-09-457-568-26	Sequence 26, Appli
19	931	88.6	198	US-09-457-568-26	Sequence 26, Appli
20	926	88.1	391	US-08-589-981-2	Sequence 2, Appli
21	926	88.1	391	US-09-457-568-4	Sequence 4, Appli
22	924	87.9	198	US-08-275-983B-3	Sequence 3, Appli
23	924	87.9	198	US-09-457-568-10	Sequence 10, Appli
24	921	87.6	365	US-09-457-568-10	Sequence 10, Appli
25	921	87.6	380	US-09-457-568-8	Sequence 8, Appli
26	921	87.6	380	US-09-457-568-8	Sequence 8, Appli
27	921	87.6	380	US-09-457-568-8	Sequence 8, Appli

28	919	87.4	198	US-08-854-039B-2	Sequence 2, Appli
29	914	87.0	365	US-09-457-568-6	Sequence 6, Appli
30	914	87.0	365	US-09-457-568-6	Sequence 6, Appli
31	855	81.4	178	US-08-794-002-6	Sequence 6, Appli
32	855	81.4	178	US-08-854-039B-6	Sequence 6, Appli
33	855	81.4	198	US-08-275-983B-1	Sequence 1, Appli
34	855	81.4	198	US-08-794-002-2	Sequence 2, Appli
35	789	75.1	334	US-09-457-568-15	Sequence 15, Appli
36	789	75.1	334	US-09-457-568-14	Sequence 14, Appli
37	787.5	74.9	348	US-09-457-568-14	Sequence 14, Appli
38	787.5	74.9	348	US-09-457-568-14	Sequence 14, Appli
39	784	74.6	177	US-09-457-568-12	Sequence 12, Appli
40	784	74.6	177	US-09-457-568-12	Sequence 12, Appli
41	714	69.4	197	US-09-215-221-55	Sequence 55, Appli
42	392	37.3	237	US-09-457-568-20	Sequence 20, Appli
43	392	37.3	237	US-09-457-568-20	Sequence 20, Appli
44	390	37.1	80	US-09-457-568-18	Sequence 18, Appli
45	390	37.1	80	US-09-457-568-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1
US-08-275-983B-2
Sequence 2, Application US/08275983B
Patent No. 568665
GENERAL INFORMATION:
APPLICANT: Massague, Joan
APPLICANT: Roberts, James M.
APPLICANT: Koff, Andrew
APPLICANT: Foltak, Kornelia
TITLE OF INVENTION: Isolated p27 protein, Nucleic Acid Molecules
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
AUERSEE, IAHIVE & LOCKFIELD
STREET, 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/275,983B
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/179,045
FILING DATE: 07-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/INCKET NUMBER: M1-079CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO.: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-08-275-983B-2

Query Match: 100.0%; Score 1051; DB 1; Length 197;
Best Local Similarity: 100.0%; Pred. No. 2.5e+102;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 2 5e-102;
Matches 197; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSNVAVSNGSPSLERFMARQADHPKPSACRNLEGPVNHHELTJDLKHKRQMEASQPKW 60
DB 1 MSNVAVSNGSPSLERFMARQADHPKPSACRNLEGPVNHHELTJDLKHKRQMEASQPKW 60
QY 61 NFDQNHKPLEGRYEMQVEVERGSLPEFYRPPRPKRSACKVLAQESQDVSGSRQAVPLIG 120
DB 61 NFDQNHKPLEGRYEMQVEVERGSLPEFYRPPRPKRSACKVLAQESQDVSGSRQAVPLIG 120
QY 121 SQANSEDRHLVDQMPDSDNOAGLAECQCGMKRRPAEDSSONKRPANTEEVSQSGFN 180
DB 121 SQANSEDRHLVDQMPDSDNOAGLAECQCGMKRRPAEDSSONKRPANTEEVSQSGFN 180
QY 181 ACTIVEOTPKKPGRLROT 197
DB 181 ACTIVEOTPKKPGRLROT 197

RESULT 5

US-08-854-039B-4
Sequence 4, Application US/08854039B
Patent No. 6355774
GENERAL INFORMATION:
APPLICANT: Massague, Joan
APPLICANT: Roberts, James M.
APPLICANT: Koff, Andrew
APPLICANT: Polyak, Kornelia
TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS
NUMBER OF INVENTIONS: PRODUCTION AND USE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,039B
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-079.04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ. ID NO.: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-854-039B-4

Query Match 99.1%; Score 1042; DB 4; Length 197;

Best Local Similarity 99.5%; Pred. No. 2 2e-101;
Matches 196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNVAVSNGSPSLERFMARQADHPKPSACRNLEGPVNHHELTJDLKHKRQMEASQPKW 60
DB 1 MSNVAVSNGSPSLERFMARQADHPKPSACRNLEGPVNHHELTJDLKHKRQMEASQPKW 60
QY 61 NFDQNHKPLEGRYEMQVEVERGSLPEFYRPPRPKRSACKVLAQESQDVSGSRQAVPLIG 120
DB 61 NFDQNHKPLEGRYEMQVEVERGSLPEFYRPPRPKRSACKVLAQESQDVSGSRQAVPLIG 120
QY 121 SQANSEDRHLVDQMPDSDNOAGLAECQCGMKRRPAEDSSONKRPANTEEVSQSGFN 180
DB 121 SQANSEDRHLVDQMPDSDNOAGLAECQCGMKRRPAEDSSONKRPANTEEVSQSGFN 180
QY 181 ACTIVEOTPKKPGRLROT 197
DB 181 ACTIVEOTPKKPGRLROT 197

QY 121 SQANSEDRHLVDQMPDSDNOAGLAECQCGMKRRPAEDSSONKRPANTEEVSQSGFN 180
DB 121 SQANSEDRHLVDQMPDSDNOAGLAECQCGMKRRPAEDSSONKRPANTEEVSQSGFN 180
QY 181 ACTIVEOTPKKPGRLROT 197
DB 181 ACTIVEOTPKKPGRLROT 197

RESULT 6

US-08-415-655-6
Sequence 6, Application US/08415655
Patent No. 6023480
GENERAL INFORMATION:
APPLICANT: Massague, Joan
APPLICANT: Lee, Mong-hong
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: p75K1P2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,655
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/47418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-5525
INFORMATION FOR SEQ. ID NO.: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-415-655-6

Query Match 99.0%; Score 1040; DB 3; Length 197;

Best Local Similarity 99.0%; Pred. No. 3 6e-101;
Matches 195; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNVAVSNGSPSLERFMARQADHPKPSACRNLEGPVNHHELTJDLKHKRQMEASQPKW 60
DB 1 MSNVAVSNGSPSLERFMARQADHPKPSACRNLEGPVNHHELTJDLKHKRQMEASQPKW 60
QY 61 NFDQNHKPLEGRYEMQVEVERGSLPEFYRPPRPKRSACKVLAQESQDVSGSRQAVPLIG 120
DB 61 NFDQNHKPLEGRYEMQVEVERGSLPEFYRPPRPKRSACKVLAQESQDVSGSRQAVPLIG 120
QY 121 SQANSEDRHLVDQMPDSDNOAGLAECQCGMKRRPAEDSSONKRPANTEEVSQSGFN 180
DB 121 SQANSEDRHLVDQMPDSDNOAGLAECQCGMKRRPAEDSSONKRPANTEEVSQSGFN 180
QY 181 ACTIVEOTPKKPGRLROT 197
DB 181 ACTIVEOTPKKPGRLROT 197

100 ACTIVE INFORMATION

RESULT 7

US 09 215 221 52

1. SUBJECT: 100 ACTIVE INFORMATION

2. PATENT No. 6,200,000

3. GENERAL INFORMATION:

4. APPLICANT: ELLERS, MARTIN

5. APPLICANT: ELLERS, ANDREA

6. TITLE OF INVENTION: METHOD AND APPARATUS FOR THE

7. FILE REFERENCE: 02/0043214

8. CURRENT APPLICATION NUMBER: 02/0043214

9. PRIOR APPLICATION NUMBER: 02/0043214

10. PRIOR FILING DATE: 1997 12 20

11. NUMBER OF SHEETS: 6

12. SOFTWARE: Patent in view 2.1

13. SHEET NO. 49

14. LENGTH: 212

15. TYPE: PAT

16. ORGANISM: Mammals

17. FEATURE:

18. OTHER INFORMATION: Description of Active Information

US 09 215 221 49

100 ACTIVE INFORMATION

RESULT 8

US 09 215 221 52

1. SUBJECT: 100 ACTIVE INFORMATION

2. PATENT No. 6,200,000

3. GENERAL INFORMATION:

4. APPLICANT: ELLERS, MARTIN

5. APPLICANT: ELLERS, ANDREA

6. TITLE OF INVENTION: METHOD AND APPARATUS FOR THE

7. FILE REFERENCE: 02/0043214

8. CURRENT APPLICATION NUMBER: 02/0043214

9. PRIOR APPLICATION NUMBER: 02/0043214

10. PRIOR FILING DATE: 1997 12 20

11. NUMBER OF SHEETS: 6

12. SOFTWARE: Patent in view 2.1

13. SHEET NO. 52

14. LENGTH: 194

15. TYPE: PAT

16. ORGANISM: Mammals

17. FEATURE:

18. OTHER INFORMATION: Description of Active Information

US 09 215 221 52

100 ACTIVE INFORMATION

RESULT 9

US 09 215 221 52

1. SUBJECT: 100 ACTIVE INFORMATION

2. PATENT No. 6,200,000

3. GENERAL INFORMATION:

4. APPLICANT: ELLERS, MARTIN

5. APPLICANT: ELLERS, ANDREA

6. TITLE OF INVENTION: METHOD AND APPARATUS FOR THE

7. FILE REFERENCE: 02/0043214

8. CURRENT APPLICATION NUMBER: 02/0043214

9. PRIOR APPLICATION NUMBER: 02/0043214

10. PRIOR FILING DATE: 1997 12 20

11. NUMBER OF SHEETS: 6

12. SOFTWARE: Patent in view 2.1

13. SHEET NO. 52

14. LENGTH: 194

15. TYPE: PAT

16. ORGANISM: Mammals

17. FEATURE:

18. OTHER INFORMATION: Description of Active Information

US 09 215 221 52

100 ACTIVE INFORMATION

100 ACTIVE INFORMATION

RESULT 10

US 09 215 221 54

1. SUBJECT: 100 ACTIVE INFORMATION

2. PATENT No. 6,200,000

3. GENERAL INFORMATION:

4. APPLICANT: ELLERS, MARTIN

5. APPLICANT: ELLERS, ANDREA

6. TITLE OF INVENTION: METHOD AND APPARATUS FOR THE

7. FILE REFERENCE: 02/0043214

8. CURRENT APPLICATION NUMBER: 02/0043214

9. PRIOR APPLICATION NUMBER: 02/0043214

10. PRIOR FILING DATE: 1997 12 20

11. NUMBER OF SHEETS: 6

12. SOFTWARE: Patent in view 2.1

13. SHEET NO. 54

14. LENGTH: 194

15. TYPE: PAT

16. ORGANISM: Mammals

17. FEATURE:

18. OTHER INFORMATION: Description of Active Information

US 09 215 221 54

100 ACTIVE INFORMATION

RESULT 11

US 09 215 221 54

1. SUBJECT: 100 ACTIVE INFORMATION

2. PATENT No. 6,200,000

3. GENERAL INFORMATION:

4. APPLICANT: ELLERS, MARTIN

5. APPLICANT: ELLERS, ANDREA

6. TITLE OF INVENTION: METHOD AND APPARATUS FOR THE

7. FILE REFERENCE: 02/0043214

8. CURRENT APPLICATION NUMBER: 02/0043214

9. PRIOR APPLICATION NUMBER: 02/0043214

10. PRIOR FILING DATE: 1997 12 20

11. NUMBER OF SHEETS: 6

12. SOFTWARE: Patent in view 2.1

13. SHEET NO. 54

14. LENGTH: 194

15. TYPE: PAT

16. ORGANISM: Mammals

17. FEATURE:

18. OTHER INFORMATION: Description of Active Information

US 09 215 221 54

100 ACTIVE INFORMATION

RESULT 12

US 09 215 221 54

1. SUBJECT: 100 ACTIVE INFORMATION

2. PATENT No. 6,200,000

3. GENERAL INFORMATION:

4. APPLICANT: ELLERS, MARTIN

5. APPLICANT: ELLERS, ANDREA

6. TITLE OF INVENTION: METHOD AND APPARATUS FOR THE

7. FILE REFERENCE: 02/0043214

8. CURRENT APPLICATION NUMBER: 02/0043214

9. PRIOR APPLICATION NUMBER: 02/0043214

10. PRIOR FILING DATE: 1997 12 20

11. NUMBER OF SHEETS: 6

12. SOFTWARE: Patent in view 2.1

13. SHEET NO. 54

14. LENGTH: 194

15. TYPE: PAT

16. ORGANISM: Mammals

17. FEATURE:

18. OTHER INFORMATION: Description of Active Information

US 09 215 221 54

100 ACTIVE INFORMATION

```

? APPLICANT: EILERS, MARTIN
? APPLICANT: BIERGIN, ANDREA
? APPLICANT: SEDLACEK, HANS-HARALD
? TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
? TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
? FILE REFERENCE: 026083/0192
? CURRENT APPLICATION NUMBER: US/09/215,221
? CURRENT FILING DATE: 1998-12-18
? PRIOR FILING DATE: 1997-12-20
? NUMBER OF SEQ ID NOS: 57
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 54
? LENGTH: 195
? TYPE: PRT
? ORGANISM: Murine sp
? FEATURE:
? OTHER INFORMATION: mutated p27
US-09-215-221-54

```

```

Query Match          95.5%: Score 1003.5; DB 4; Length 195;
Best Local Similarity 97.9%; Pred. No. 2,3e-97;
Matches 191; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

```

```

QY 3 NVKVSNGSPLEKMDARQADHPKPSACNLEGPVNHDELTDLEKHCROMEASQKKMNF 62
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 1 NVKVSNGSPLEKMDARQADHPKPSACNLEGPVNHDELTDLEKHCROMEASQKKMNF 54
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 63 DQGNKPLEGRTKEMQVEERGSLEPEFYRPPRPKPSACVLAQESQVSSKAVPLTSSQ 123
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 60 DQGNKPLEGRTKEMQVEERGSLEPEFYRPPRPKPSACVLAQESQVSSKAVPLTSSQ 119
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 123 ANSEDRHLVDQMFDSSDPAAGLAEQVQKMKKKAEDSSQNKANKTEENVSQSSPNAG 184
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 120 ANSEDRHLVDQMFDSSDPAAGLAEQVQKMKKKAEDSSQNKANKTEENVSQSSPNAG 179
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 183 TVEQTPKKRGLRRQT 197
   ||||||||||||||||
DB 180 TVEQTPKKRGLRRQT 194

```

```

RESULT 11
US-09-215-221-51
? Sequence 51, Application US/09215221
? Patent No. 6265562
? GENERAL INFORMATION:
? APPLICANT: EILERS, MARTIN
? APPLICANT: BIERGIN, ANDREA
? APPLICANT: SEDLACEK, HANS-HARALD
? TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
? TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
? FILE REFERENCE: 026083/0192
? CURRENT APPLICATION NUMBER: US/09/215,221
? CURRENT FILING DATE: 1998-12-18
? PRIOR FILING DATE: 1997-12-20
? NUMBER OF SEQ ID NOS: 57
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 51
? LENGTH: 194
? TYPE: PRT
? ORGANISM: Murine sp.
? FEATURE:
? OTHER INFORMATION: mutated p27
US-09-215-221-51

```

```

Query Match          94.5%: Score 994; DB 4; Length 194;
Best Local Similarity 96.9%; Pred. No. 2,3e-96;
Matches 187; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```

```

QY 5 PVSNGSPLEPMARQADHPKPSACNLEGPVNHDELTDLEKHCROMEASQKKMNF 64
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 1 RVSNOSPSPERMDARQADHPKPSACNLEGPVNHDELTDLEKHCROMEASQKKMNF 60

```

```

QY 65 QNKRPLEGRTKEMQVEERGSLEPEFYRPPRPKPSACVLAQESQVSSKAVPLTSSQ 124
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 61 QNKRPLEGRTKEMQVEERGSLEPEFYRPPRPKPSACVLAQESQVSSKAVPLTSSQ 120
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 125 SEDRLVDQMFDSSDPAAGLAEQVQKMKKKAEDSSQNKANKTEENVSQSSPNAG 184
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 121 SEDRLVDQMFDSSDPAAGLAEQVQKMKKKAEDSSQNKANKTEENVSQSSPNAG 180
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 185 EQTPKKRGLRRQT 197
   ||||||||||||||||
DB 181 EQTPKKRGLRRQT 193

```

```

RESULT 12
US-09-215-221-55
? Sequence 55, Application US/09215221
? Patent No. 6265562
? GENERAL INFORMATION:
? APPLICANT: EILERS, MARTIN
? APPLICANT: BIERGIN, ANDREA
? APPLICANT: SEDLACEK, HANS-HARALD
? TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
? TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
? FILE REFERENCE: 026083/0192
? CURRENT APPLICATION NUMBER: US/09/215,221
? CURRENT FILING DATE: 1998-12-18
? PRIOR FILING DATE: 1997-12-20
? NUMBER OF SEQ ID NOS: 57
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 55
? LENGTH: 180
? TYPE: PRT
? ORGANISM: Murine sp.
? FEATURE:
? OTHER INFORMATION: mutated p27
US-09-215-221-55

```

```

Query Match          90.2%: Score 948; DB 4; Length 180;
Best Local Similarity 98.3%; Pred. No. 1,3e-91;
Matches 177; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 16 MIAWALHPKPSACNLEGPVNHDELTDLEKHCROMEASQKKMNFQNPVNHDELGRYE 75
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 1 MIAWALHPKPSACNLEGPVNHDELTDLEKHCROMEASQKKMNFQNPVNHDELGRYE 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 76 WOEVERGSTPEFYRPPRPKPSACVLAQESQVSSKAVPLTSSQSSPNAG 135
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 61 WOEVERGSTPEFYRPPRPKPSACVLAQESQVSSKAVPLTSSQSSPNAG 120
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 136 QNKRPLEGRTKEMQVEERGSLEPEFYRPPRPKPSACVLAQESQVSSKAVPLTSSQ 195
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 121 QNKRPLEGRTKEMQVEERGSLEPEFYRPPRPKPSACVLAQESQVSSKAVPLTSSQ 180
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```

```

RESULT 13
US-09-215-221-50
? Sequence 50, Application US/09215221
? Patent No. 6265562
? GENERAL INFORMATION:
? APPLICANT: EILERS, MARTIN
? APPLICANT: BIERGIN, ANDREA
? APPLICANT: SEDLACEK, HANS-HARALD
? TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
? TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
? FILE REFERENCE: 026083/0192
? CURRENT APPLICATION NUMBER: US/09/215,221
? CURRENT FILING DATE: 1998-12-18
? PRIOR FILING DATE: 1997-12-20
? NUMBER OF SEQ ID NOS: 57
? SOFTWARE: PatentIn Ver. 2.1

```

```

1  SEQID: No 50
2  LENGTH: 180
3  TYPE: prt
4  ORGANISM: Mus mus sp
5  FEATURE:
6  OTHER INFORMATION: Not annotated
7  OS: 09.215.221.50

```

[illegible][illegible]

RESULT 14
US/08-406,248-4
See Question 4, Appendix A, US/08-406,248-4

GENERAL INFORMATION
APPLICANT: Murogi Kaiti
APPLICANT: Address: 3, Ito-cho
TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING
TITLE OF INVENTION: TRANSPORTED CELLS
NUMBER OF SEQUENCE: 6
CORRESPONDENT ADDRESS:
ADDRESS: AND TADAHI KIMOTO, Ph.D., Ippin 8 Kusunoki
CITY: 20-1-10, Street

[illegible]

ATTORNEY/AGENT INFORMATION:
NAME: MULLOOLS PATRICIA A.
REGISTRATION NUMBER: 44-104
REFERENCE/BOOK NUMBER: 004-011
IDENTIFICATION NUMBER:
TELEPHONE: 617-860-1400
TELEFAX: 617-860-1411

```

1 INFORMATION FOR SEQ 4
2 SEQUENCE CHARACTERISTICS
3 LENGTH: 196 amino acids
4 TYPE: amino acid
5 topology: none
6 MOLECULE TYPE: protein
7 UNK ON: 406, 240, 4

```

Query Match	00.6%	Score 941	08.1%	Length 1987
Post Local Similarity	0.00%	Prod N = 9	10.9%	
Matches 1/2	0.0000000	1.2	Matches 1.8	Matches 0.0

[illegible]

Protein	Accession	Length (aa)	PI	MW (kDa)	Ref.
1	ADAMTS-1	1000	5.5	120	[1]
2	ADAMTS-2	1000	5.5	120	[2]
3	ADAMTS-3	1000	5.5	120	[3]
4	ADAMTS-4	1000	5.5	120	[4]
5	ADAMTS-5	1000	5.5	120	[5]
6	ADAMTS-6	1000	5.5	120	[6]
7	ADAMTS-7	1000	5.5	120	[7]
8	ADAMTS-8	1000	5.5	120	[8]
9	ADAMTS-9	1000	5.5	120	[9]
10	ADAMTS-10	1000	5.5	120	[10]
11	ADAMTS-11	1000	5.5	120	[11]
12	ADAMTS-12	1000	5.5	120	[12]
13	ADAMTS-13	1000	5.5	120	[13]
14	ADAMTS-14	1000	5.5	120	[14]
15	ADAMTS-15	1000	5.5	120	[15]
16	ADAMTS-16	1000	5.5	120	[16]
17	ADAMTS-17	1000	5.5	120	[17]
18	ADAMTS-18	1000	5.5	120	[18]
19	ADAMTS-19	1000	5.5	120	[19]
20	ADAMTS-20	1000	5.5	120	[20]
21	ADAMTS-21	1000	5.5	120	[21]
22	ADAMTS-22	1000	5.5	120	[22]
23	ADAMTS-23	1000	5.5	120	[23]
24	ADAMTS-24	1000	5.5	120	[24]
25	ADAMTS-25	1000	5.5	120	[25]
26	ADAMTS-26	1000	5.5	120	[26]
27	ADAMTS-27	1000	5.5	120	[27]
28	ADAMTS-28	1000	5.5	120	[28]
29	ADAMTS-29	1000	5.5	120	[29]
30	ADAMTS-30	1000	5.5	120	[30]
31	ADAMTS-31	1000	5.5	120	[31]
32	ADAMTS-32	1000	5.5	120	[32]
33	ADAMTS-33	1000	5.5	120	[33]
34	ADAMTS-34	1000	5.5	120	[34]
35	ADAMTS-35	1000	5.5	120	[35]
36	ADAMTS-36	1000	5.5	120	[36]
37	ADAMTS-37	1000	5.5	120	[37]
38	ADAMTS-38	1000	5.5	120	[38]
39	ADAMTS-39	1000	5.5	120	[39]
40	ADAMTS-40	1000	5.5	120	[40]
41	ADAMTS-41	1000	5.5	120	[41]
42	ADAMTS-42	1000	5.5	120	[42]
43	ADAMTS-43	1000	5.5	120	[43]
44	ADAMTS-44	1000	5.5	120	[44]
45	ADAMTS-45	1000	5.5	120	[45]
46	ADAMTS-46	1000	5.5	120	[46]
47	ADAMTS-47	1000	5.5	120	[47]
48	ADAMTS-48	1000	5.5	120	[48]
49	ADAMTS-49	1000	5.5	120	[49]
50	ADAMTS-50	1000	5.5	120	[50]
51	ADAMTS-51	1000	5.5	120	[51]
52	ADAMTS-52	1000	5.5	120	[52]
53	ADAMTS-53	1000	5.5	120	[53]
54	ADAMTS-54	1000	5.5	120	[54]
55	ADAMTS-55	1000	5.5	120	[55]
56	ADAMTS-56	1000	5.5	120	[56]
57	ADAMTS-57	1000	5.5	120	[57]
58	ADAMTS-58	1000	5.5	120	[58]
59	ADAMTS-59	1000	5.5	120	[59]
60	ADAMTS-60	1000	5.5	120	[60]
61	ADAMTS-61	1000	5.5	120	[61]
62	ADAMTS-62	1000	5.5	120	[62]
63	ADAMTS-63	1000	5.5	120	[63]
64	ADAMTS-64	1000	5.5	120	[64]
65	ADAMTS-65				

1. RESOLUTION 11
 2. DIS. FOR 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675,

	Query Match	88.6%	Score 9.31	Ref. 4	Length 190
Host Local Similarity	87.0%	Prod. No. 9,416	100%		
Matches 1/22	Forwarded 1/20	11	Matches 1/21	Forwarded 1/19	

[illegible]

Source: compiled by Mary Jo, 2000. 09-03-04
 File name: 4-762-1005

GenCore version 5.1.6
Copyright (c) 1994 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: May 30, 2003, 08:58:12 ; Search time 20.1072 Seconds
(without alignments)
991.736 Million cell updates/sec

Title: US-09-865-018B-4

Perfect score: 1051
Sequence: 1 MSNVRVSGSPSLERMDAPQ SPNAGTVECTPKKPGILPPT 197

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0
Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Published_Applications_AA*

1:	/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2:	/cgn2_6/ptodata/1/pubpaa/PC01_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/1/pubpaa/US06_PUB.pep.*
5:	/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6:	/cgn2_6/ptodata/1/pubpaa/US07_PUB.pep.*
7:	/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
8:	/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9:	/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10:	/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11:	/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12:	/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1042	99.1	197	US-09-865-018-4	Sequence 4, Appl
2	931	88.6	198	US-09-970-561-2	Sequence 2, Appl
3	926	88.1	191	US-08-902-572-2	Sequence 2, Appl
4	921	87.6	195	US-08-902-572-8	Sequence 8, Appl
5	921	87.6	180	US-08-902-572-6	Sequence 6, Appl
6	919	87.4	194	US-09-865-018-2	Sequence 2, Appl
7	855	81.4	178	US-09-865-018-6	Sequence 6, Appl
8	789	75.1	334	US-08-902-572-22	Sequence 22, Appl
9	787	74.9	348	US-08-902-572-24	Sequence 24, Appl
10	784	74.6	167	US-08-902-572-18	Sequence 18, Appl
11	392	47.3	237	US-08-902-572-27	Sequence 27, Appl
12	390	37.1	252	US-08-902-572-28	Sequence 28, Appl
13	383	36.4	70	US-08-902-572-20	Sequence 20, Appl
14	194	15.5	247	US-09-945-297-770	Sequence 770, App
15	163	15.5	164	US-09-221-268-3	Sequence 2, Appl
16	163	15.5	164	US-09-221-268-5	Sequence 2, Appl
17	163	15.5	164	US-09-865-018-24	Sequence 24, Appl
18	163	15.5	164	US-09-940-766-2	Sequence 2, Appl
19	103	9.8	191	US-09-733-507-2	Sequence 2, Appl

20	103	9.8	191	US-09-733-507-10	Sequence 10, Appl
21	96	9.1	520	US-09-945-848-14	Sequence 14, Appl
22	89.5	8.5	212	US-09-233-509-12	Sequence 12, Appl
23	89	8.5	265	US-09-864-751-34248	Sequence 34248, A
24	86	8.2	405	US-09-949-407-64	Sequence 63, Appl
25	85.5	8.1	472	US-09-953-407-2	Sequence 2, Appl
26	85.5	8.1	1429	US-09-953-407-1	Sequence 1, Appl
27	82	8.1	137	US-09-733-507-14	Sequence 14, Appl
28	85	8.1	461	US-09-945-848-2	Sequence 2, Appl
29	85	8.1	1205	US-10-164-890-1	Sequence 1, Appl
30	84.5	8.0	314	US-09-764-826-44	Sequence 43, Appl
31	84.5	8.0	670	US-09-843-187-86	Sequence 86, Appl
32	84.5	8.0	671	US-10-174-590-346	Sequence 346, Appl
33	84.5	8.0	671	US-10-176-758-346	Sequence 346, Appl
34	84.5	8.0	671	US-10-175-737-346	Sequence 346, Appl
35	84.5	8.0	671	US-10-173-706-346	Sequence 346, Appl
36	84.5	8.0	671	US-10-175-738-346	Sequence 346, Appl
37	84.5	8.0	671	US-10-175-752-346	Sequence 346, Appl
38	84.5	8.0	671	US-10-176-482-346	Sequence 346, Appl
39	84.5	8.0	671	US-10-176-757-346	Sequence 346, Appl
40	84.5	8.0	671	US-10-176-913-346	Sequence 346, Appl
41	84.5	8.0	671	US-10-180-552-346	Sequence 346, Appl
42	84.5	8.0	671	US-10-180-557-346	Sequence 346, Appl
43	84.5	8.0	671	US-10-173-700-346	Sequence 346, Appl
44	84.5	8.0	671	US-10-174-572-346	Sequence 346, Appl
45	84.5	8.0	671	US-10-174-579-346	Sequence 346, Appl

ALIGNMENTS

RESULT 1
US-09-865-018-4
Sequence 4, Application US/09865018
Patent No. US200110846A1

GENERAL INFORMATION:
APPLICANT: Massague, Joan
Koff, Andrew
Roberts, James M.

TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS PRODUCTION AND USE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
ADDRESS: POLEY, HOAG & ELLIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatibale
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentlin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/865,018
FILING DATE: 24 May 2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/865,018
FILING DATE: 09 May 1997

ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Kathleen P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-079, 04
TELEPHONE: 617-833-1000
TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
TOPOLOGY: linear

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/902,572
FILING DATE: 29-JUL-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-069,03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-7000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ. ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-902-572-8

Query Match: 87.6%, Score 921, DB 8, Length 365,
Best Local Similarity 87.2%, Pred. No. 4,5e-73;
Matches 170; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 2 SNVSVNSPSLEPMARQADHPKPSACPNLFGPVNHETLPLEKHCPMFPASQPKWN 61
DB 169 SNVSVNSPSLEPMARQADHPKPSACPNLFGPVNHETLPLEKHCPMFPASQPKWN 228
QY 62 FDFQNHKPLEGKYEWEVERGSLPEFYPPPPPKPSACVLAQESQVSSPQAVPLTGS 121
DB 229 FDFQNHKPLEGKYEWEVERGSLPEFYPPPPPKPSACVLAQESQVSSPQAVPLTGS 288
QY 122 QANSEDRHLVDMPPSSDQACLAEGCPCGMKKKPPAAELSSSSONKANRTEENVSSGSPNA 181
DB 289 QANSEDRHLVDMPPSSDQACLAEGCPCGMKKKPPAAELSSSSONKANRTEENVSSGSPNA 348
QY 182 GTVEQTPKKPGLRRQ 196
DB 349 GSVEQTPKKPGLRRR 363

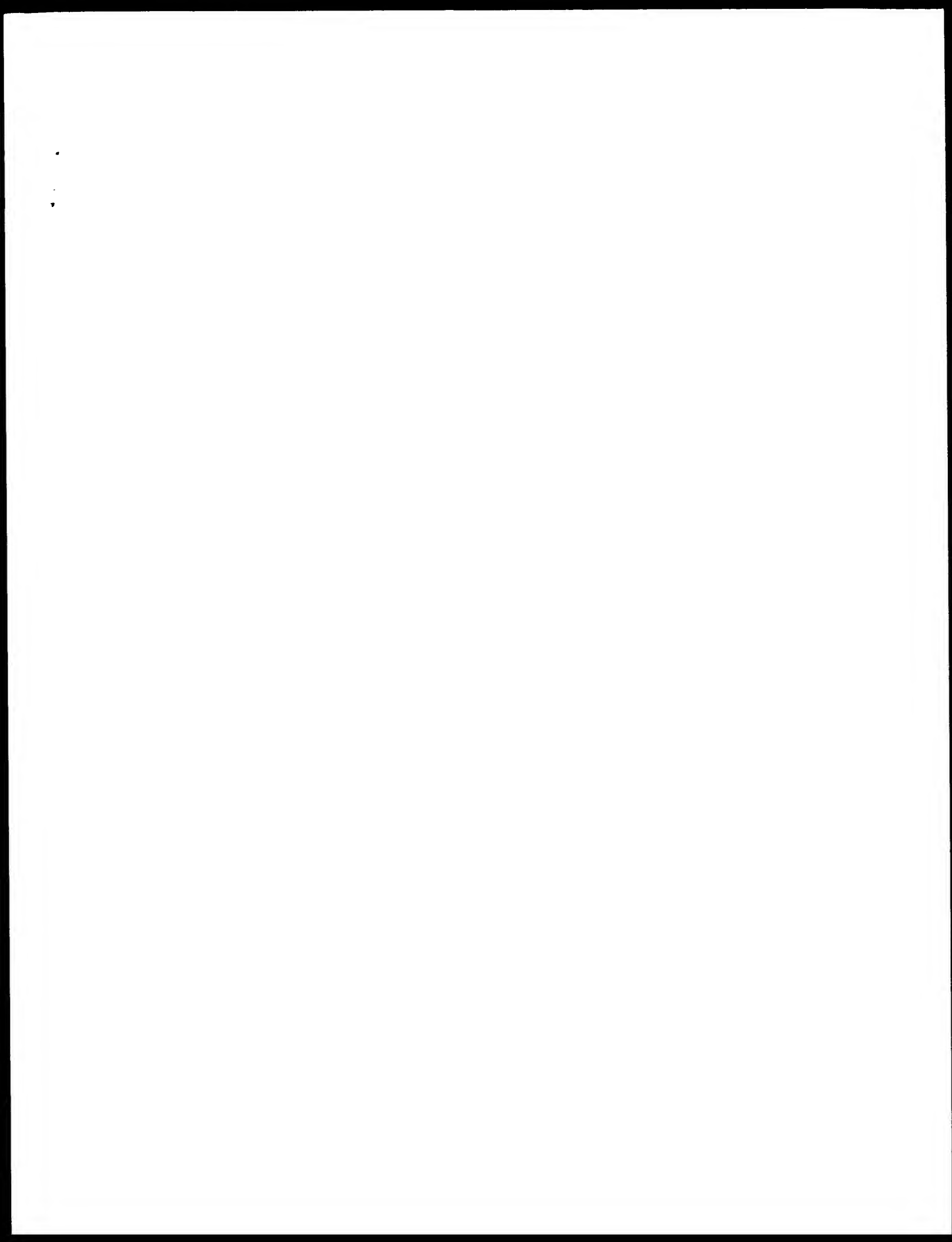
RESULT 5
US-08-902-572-6
Sequence 6, Application US/08902572
Patent No. US20020068706A1
GENERAL INFORMATION:
APPLICANT: Gyuris, Jeno
APPLICANT: Lamphere, Lou
APPLICANT: Beach, David H.
TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/902,572
FILING DATE: 29-JUL-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-069,03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-7000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-902-572-6

Query Match: 87.6%, Score 921, DB 8, Length 380,
Best Local Similarity 87.2%, Pred. No. 4,7e-73;
Matches 170; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 2 SNVSVNSPSLEPMARQADHPKPSACPNLFGPVNHETLPLEKHCPMFPASQPKWN 61
DB 184 SNVSVNSPSLEPMARQADHPKPSACPNLFGPVNHETLPLEKHCPMFPASQPKWN 243
QY 62 FDFQNHKPLEGKYEWEVERGSLPEFYPPPPPKPSACVLAQESQVSSPQAVPLTGS 121
DB 244 FDFQNHKPLEGKYEWEVERGSLPEFYPPPPPKPSACVLAQESQVSSPQAVPLTGS 303
QY 122 QANSEDRHLVDMPPSSDQACLAEGCPCGMKKKPPAAELSSSSONKANRTEENVSSGSPNA 181
DB 364 QANSEDRHLVDMPPSSDQACLAEGCPCGMKKKPPAAELSSSSONKANRTEENVSSGSPNA 363
QY 182 GTVEQTPKKPGLRRQ 196
DB 364 GSVEQTPKKPGLRRR 378

RESULT 6
US-09-865-018-2
Sequence 2, Application US/09865018
Patent No. US2002011086A1
GENERAL INFORMATION:
APPLICANT: Massague, Joan
APPLICANT: Roberts, James M.
APPLICANT: Koff, Andrew
APPLICANT: Polyak, Korneelia
TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHOD FOR ITS
PRODUCTION AND USE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109 2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,018
FILING DATE: 24-May-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,039
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-079,04



GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 08:54.42, Search time 16.5419 seconds
(without alignments)
1144.739 Million cell updates/sec

Title: US-09-865-018B-4

Perfect score: 1051
Sequence: 1 MSNVFVNSGSPLEPMARQ.....SPNAGTYEQIPKKRGLRKQT 197

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1051	100.0	197	149064	cyclin-cdk inhibit
2	928	88.3	198	152718	gene p27Kip1 prote
3	220	20.9	210	151683	cyclin-dependent k
4	211.5	20.1	348	149262	cyclin-cdk inhibit
5	196.5	18.7	316	G02424	cyclin-dependent k
6	182	17.3	164	184725	tumor suppressor p
7	174.5	16.6	159	149023	p53 tumor suppress
8	171.5	16.3	143	A49438	cyclin-dependent k
9	164	15.6	181	168674	cyclin-dependent k
10	162	15.4	281	154380	hypothetical prote
11	141.5	13.5	258	T24499	hypothetical prote
12	117	11.1	184	T24496	hypothetical prote
13	103	9.8	191	T01132	cyclin-dependent k
14	96	9.1	1277	T32731	PAR interacting pr
15	95.5	9.1	570	A97238	membrane associat
16	94.5	9.0	1045	T18373	erythrocyte bindin
17	94.5	9.0	1211	T43230	hypothetical prote
18	92.5	8.8	290	T32161	histone deacetylase
19	92.5	8.8	296	T48401	AF-4 protein - mou
20	92.5	8.8	1217	T42625	Invulvulin - fig-
21	92	8.8	450	A47731	NSD1 protein - mou
22	91.5	8.7	2588	T14342	protein kinase (EC
23	90.5	8.6	768	H54024	protein kinase (EC
24	90.5	8.6	777	B54024	protein kinase (EC
25	90.5	8.6	777	F54024	protein kinase (EC
26	90.5	8.6	779	E54024	protein kinase (EC
27	90	8.6	374	C88734	protein F32E10.6 [
28	89.5	8.5	575	A63716	spore coat assemb
29	89.5	8.5	1205	T13959	timeless protein T

30	89	8.5	783	A55817	cyclin-dependent k
31	89	8.5	1307	T25563	hypothetical prote
32	88.5	8.4	372	S23326	gene M2.2 protein
33	88	8.4	246	S49770	hypothetical prote
34	86.5	8.2	525	T27194	cd32A - rat
35	86.5	8.2	607	A43776	drebrin E2 - chick
36	86.5	8.2	694	AF2251	AF2251
37	86.5	8.2	701	S17196	transcription fact
38	86.5	8.2	919	A41275	DNA ligase (ATP)
39	86.5	8.2	1004	H88562	protein G07A9.3 [1
40	86.5	8.2	1044	S40704	hypothetical prote
41	86.5	8.2	1173	T42719	TBR-coat-inhib/SH2
42	86	8.2	383	A48232	domain 48K chain
43	86	8.2	495	T43902	domain 52K chain
44	86	8.2	611	S12566	translation initia
45	85.5	8.1	536	H72535	hypothetical prote

ALIGNMENTS

RESULT 1
149064
cyclin-cdk inhibitor p27 - mouse
N:Alternate names: CDI p27; G1 cyclin-cyclin-dependent kinase inhibitor p27
C:Species: Mus musculus (house mouse)
C>Date: 09-Mar-1996 #sequence, revision 09-Mar-1996 #text, change 05-Nov-1999
C:Accession: 149064
R:Toyoshima, H.; Hunter, T.
Cell 78, 67-74, 1994
A>Title: p27, a novel inhibitor of G1 cyclin-cdk protein kinase activity, is related
A:Reference number: A54839; MIM:64306510; PMID:6043213
A:Accession: 149064
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-197 <RES>
A:Cross-references: EMBL:U06440, NID:J532771, JID:AM21145.1, EIL:9532772
C:Keywords: cell cycle control

Query Match 100.0%; Score 1051; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.9e-80;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSNVFVNSGSPLEPMARQADHPKPSACPNLCFVNVHEELTPDLKRPDPMEASQPMW	60
DB	1	MSNVFVNSGSPLEPMARQADHPKPSACPNLCFVNVHEELTPDLKRPDPMEASQPMW	60
QY	61	NFQFQNHKPLBSPYEMQLFVFRGSLPEFYRPPPPPPSAKVLAQPSQVNSGSKQAVPI	120
DB	61	NFQFQNHKPLBSPYEMQLFVFRGSLPEFYRPPPPPPSAKVLAQPSQVNSGSKQAVPI	120
QY	121	SOANSEDRHLYDQMPVSSQVAGIARQCPQMKRPPAPRISSSQNKPAKPPFENVSGSPN	180
DB	121	SOANSEDRHLYDQMPVSSQVAGIARQCPQMKRPPAPRISSSQNKPAKPPFENVSGSPN	180
QY	181	AGTVEQTPKKRGLRKQT	197
DB	181	AGTVEQTPKKRGLRKQT	197

RESULT 2
152718
gene p27Kip1 protein - human
C:Species: Homo sapiens (man)
C>Date: 01-Nov-1997 #sequence, revision 01-Nov-1997 #text, change 01-Jul-2000
C:Accession: 152718
R:Platenberg, J.A.; Faldutsky, S.K.; Salov, Y.; Papadopoulos, N.; Liu, K.; Friedman, C.; Cancer Res. 55, 1206-1210, 1995
A>Title: Assignment of the human p27Kip1 gene to 12p13 and its analysis in leukemias.
A:Reference number: 152718; MIM:95188144; PMID:7882409
A:Accession: 152718
A:Status: preliminary
A:Molecule type: DNA
A:Molecule type: DNA

QY 177 -GSPNACTVEQTPPK 190
 Db 299 SAAPGVSGVEQTPPK 313

RESULT 6

184725
 Tumor suppressor p21 WAF1/CIP1 (imported) - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Jun-2000
 C:Accession: 184725
 R:El-Deiry, W.S.; Tokino, T.; Waldman, T.; Velculescu, V.; Oliver, J.D.; Burrell, M.; Hill
 Cancer Res. 55, 2910-2919, 1995
 A:Title: Topological control of p21WAF1/CIP1 expression in normal and neoplastic tissues
 A:Reference number: 149296; PMID:95316868; PMID:7796420
 A:Accession: 184725
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-164 <RES>
 A:Cross-references: EMBL:024174; NID:9302581; PDB:AA052221; FID:9302582
 A:Genetics:
 A:Gene: WAF1

Query Match 17.3%, Score 182, DB 2, Length 164,
 Best Local Similarity 28.8%, Pred. No. 4e-08;
 Matches 46, Conservative 23, Mismatches 65, Indels 26, Gaps 4;

QY 17 DAPQDHPKPSACRPIFPVNHHELTIRLEKRPDMFASQKKNNPKPIEGYEW 76

Db 6 DVPVPH-PSKVPRI-FSPVNSFQISPIKDALMASCIQFAPFNNFPAETPLEGNYW 64

QY 77 QVEVGS-LPEFYVYHFKFKSACKVLAESQVSSKAVPLGSOANSELPNI-VLQMP 146

Db 65 EKVRSPLGPKYIISP-----GSRPRDDLGDKRSTSSALLDQPGP 105

QY 137 SSDNAGLAECQPMKKKRAEUS-----SSQKKKKNPT 170

Db 106 APEDHVALSLSTLTVSHAPRPDPSPGCTGSQGRKRPOT 145

RESULT 7

149023
 Tumor suppressor p21 WAF1/CIP1 (imported) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Jun-2000
 C:Accession: 149023, 149296
 R:Huppi, K.; Swarski, L.; Dosik, J.; Muthart, P.; Choudh, M.; Reed, S.; Mark, B.; Shiv
 Oncogene 9, 3017-3020, 1994
 A:Title: Molecular cloning, sequencing, chromosomal localization and expression of mouse
 A:Reference number: 149023, PMID:94366751; PMID:8084607
 A:Accession: 149023
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-159 <RES>
 A:Cross-references: EMBL:009507; NID:959502; PDB:AA684561; FID:9535503
 R:El-Deiry, W.S.; Tokino, T.; Waldman, T.; Velculescu, V.; Oliver, J.D.; Burrell, M.; Hill
 Cancer Res. 55, 2910-2919, 1995
 A:Title: Topological control of p21WAF1/CIP1 expression in normal and neoplastic tissues
 A:Reference number: 149296, PMID:95316868, PMID:7796420
 A:Accession: 149296
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GR/EMBL
 A:Molecule type: mRNA
 A:Residues: 1-159 <RES>
 A:Cross-references: EMBL:024173; NID:9302581; PDB:AA052221; FID:9302582
 A:Genetics:
 A:Gene: WAF1

Query Match 16.6%, Score 174.5, DB 2, Length 159,
 Best Local Similarity 31.4%, Pred. No. 6e-07;
 Matches 50, Conservative 21, Mismatches 59, Indels 23, Gaps 6;
 QY 17 DAPQDHPKPSACRPIFPVNHHELTIRLEKRPDMFASQKKNNPKPIEGYEW 76

Db 6 DVPVPH-PSKVPRI-FSPVNSFQISPIKDALMASCIQFAPFNNFPAETPLEGNYW 64

QY 77 QVEVGS-LPEFYVYHFKFKSACKVLAESQVSSKAVPLGSOANSELPNI-VLQMP 146

Db 65 EKVRSPLGPKYIISP-----GSRPRDDLGDKRSTSSALLDQPGP 104

QY 137 SSDNAGLAECQPMKKKRAEUS-----SSQKKKKNPT 170

Db 106 APEDHVALSLSTLTVSHAPRPDPSPGCTGSQGRKRPOT 140

RESULT 8

149438
 p53 tumor suppressor mediator WAF1 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
 C:Accession: A49438
 R:El-Deiry, W.S.; Tokino, T.; Velculescu, V.F.; Levy, D.R.; Parsons, R.; Trent, J.M.;
 Cell 75, 817-825, 1993
 A:Title: WAF1, a putative p53 target, mediates p53 tumor suppression.
 A:Reference number: A49438, PMID:79406197; PMID:8242752
 A:Accession: A49438
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-143 <ELI>
 A:Note: sequence extracted from NIH backbone (NCBI:149807, NCBI:149808)

Query Match 16.3%, Score 171.5, DB 2, Length 143,
 Best Local Similarity 30.8%, Pred. No. 2.5e-07;
 Matches 49, Conservative 24, Mismatches 59, Indels 29, Gaps 6;

QY 17 DAPQDHPKPSACRPIFPVNHHELTIRLEKRPDMFASQKKNNPKPIEGYEW 76

Db 6 DVPVPH-PSKVPRI-FSPVNSFQISPIKDALMASCIQFAPFNNFPAETPLEGNYW 64

QY 77 QVEVGS-LPEFYVYHFKFKSACKVLAESQVSSKAVPLGSOANSELPNI-VLQMP 146

Db 65 EKVRSPLGPKYIISP-----GSRPRDDLGDKRSTSSALLDQPGP 104

QY 137 SSDNAGLAECQPMKKKRAEUS-----SSQKKKKNPT 170

Db 105 PEDHVA-LSTLTVSEPP--EDSPGPGTSGGRKRPOT 140

RESULT 9

168674
 Cyclin-dependent kinase - human (fragment)
 N:Alternate names: probable DNA synthesis inhibitor
 C:Species: Homo sapiens (man)
 C:Date: 04-Oct-1994 #sequence_revision 04-Oct-1994 #text_change 01-Dec-2000
 C:Accession: 168674; A49437; 153412; S39357
 R:Mousset, S.; Ozelick, H.; Lee, F.D.; Molkentin, D.; Bull, S.B.; Andlauer, L.L.;
 Hum Mol Genet 4, 1080-1092, 1995
 A:Title: Two variants of the CIP1/WAF1 gene occur together and are associated with hu
 A:Reference number: 154380, PMID:7594134; PMID:7659484
 A:Accession: 168674
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-181 <RES>
 A:Cross-references: EMBL:147223; NID:9086878; PDB:AA685601; PDB:9086879
 R:Harper, J.W.; Adams, C.R.; Wei, N.; Koyanari, K.; Elledge, S.J.;
 Cell 75, 805-816, 1993
 A:Title: The p21 cdk interacting protein CIP1 is a potent inhibitor of cdk cyclin-depe
 A:Reference number: A49437, PMID:7497966; PMID:8242751
 A:Accession: A49437
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 18-181 <PE3>
 A:Cross-references: EMBL:045510; NID:945512; PDB:AA610111; PDB:945513
 R:Nada, A.; Ning, Y.; Venable, S.F.; Petrella Smith, C.M.; Smith, J.R.;
 Exp. Cell Res. 211, 90-98, 1994
 A:Title: Cloning of suppressor cell derived inhibitors of DNA synthesis using an expe
 A:Reference number: 152412, PMID:9470864, PMID:8125163

OY 195 ROT 197
Db 177 TRS 179

RESULT 13

T01132
cyclin-dependent kinase inhibitor protein [imported] - Arabidopsis thaliana

N:Alternate names: hypothetical protein F26B6.8
C:Species: Arabidopsis thaliana (mouse ear cress)

C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 1b-Feb-2001

C:Accession: T01132; F84624

R:Submitted by: S.D. Kaul, S. Lin, X. Kelchum, K.A. Crosby, M.L. Hladky, R.C. Sykes,

submitted to the EMBL Data Library, June 1998

A:Description: Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence.

A:Reference number: Z14198

A:Status: translated from GB/EMBL/JRRLJ

A:Molecule type: DNA

A:Residues: 1-191 <R00>

A:Cross-references: EMBL AC003640, NID: g3242700, PID: g3242706

A:Experimental source: cultivar Columbia

R:Lin, X., Kaul, S., Rounsley, S.D., Shen, T.P., Brinkley, M.L., Powell, G., Fulton, T.Y.,

M.J. Koo, H. Moffatt, K.S. Cronin, L.A. Shen, M. VanKron, S.F. Mayhew, J. Tallon, J.

euss, D.J. Nierman, W.C. White, O.J. Eisen, J.A. Salzberg, S.L. Fraser, C.M. Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A04420, MIM: 2068497, FMTL 10617137

A:Accession: F84624

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-191 <R00>

A:Cross-references: GB: A0402043; NID: g3242700; PID: A0402043; GSP08: GSP08139

A:Gene: F26B6.8; Atg32430

A:Map position: 2

A:Introns: 66/3; 81/2; 170/2

OY 50

Db 161

161 KQLEKFKKKYNNDFEKEKLEGRYEWKIF 191

OY 50

Db 161

161

161

161

161

161

161

161

161

161

161

161

161

161

161

161

161

161

161

161

161

161

161

161

161

161

161

Db 1073 -----QAMNLLGVPRKSKKNNKVPKSSSSISTKKKK 1108

OY 150 GM-----PRPAEDSSQKRRANKTEENVSSPSNATVPTPKPRAP 146

Db 1109 GFLPFTKPKPKRLSPGTTSEKAKSQ--GVDTFPAAPATKPKPPSPKRR 1160

RESULT 15

A97238

membrane associated methyl-accepting chemotaxis protein (with HAMP domain) [imported]

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 1a-Sep-2001

C:Accession: A97238

R:Submitted by: Brereton, G., Campbell, M.V., Mariani, K.S., Tang, G., Gibson, R.J.L.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium

A:Reference number: A96909; MIM: 21459325; PMID: 21459325

A:Accession: A97238

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-570 <R00>

A:Cross-references: GB: A040437; PID: A040437; FMTL 10617137

A:Experimental source: Clostridium acetobutylicum A100824

C:Genetics:

A:Gene: CAC2746

OY 41

Db 210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

210

Search completed: May 30, 2003, 09:02:43
Job time: 18.543 secs

.

.

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 08:52:42, Search time: 4.39 sec
(without alignments)
972,808 Million cell updates/sec

Title: US-09-865-018b-4

Sequence: 1 MSNRYVSGSGSLERMDARQ.....SPNACTVEOTPKKPELRROT 197

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	1051	100.0	197	CDNB_MOUSE	P46144 mus musculus
2	962	91.5	198	CDNB_FETC	Q19001 foetus silve
3	958	91.2	198	CDNB_CRIGR	Q60439 crigolius
4	931	88.6	198	CDNB_HUMAN	P46527 homo sapien
5	855	80.1	178	CDNB_MUSVI	P46522 mustela vis
6	211.5	20.1	348	CDNC_MOUSE	P49919 mus musculu
7	196.5	18.7	316	CDNC_HUMAN	P49918 homo sapien
8	174.5	16.6	159	CDNI_MOUSE	P39689 mus musculu
9	163	15.5	164	CDNI_HUMAN	P39689 mus musculu
10	159.5	15.2	164	CDNI_FETC	Q19002 fetus silve
11	92.5	8.8	1217	AP4_MOUSE	O88573 mus musculu
12	52	8.6	450	INVL_LBMT	P14590 lemur calla
13	92	8.8	480	CDNB_HUMAN	O43193 homo sapien
14	92	8.8	1822	ZAP3_HUMAN	P49750 homo sapien
15	89.5	8.4	575	SP40_RACSO	P37663 bacillus su
16	88.5	8.4	372	M22_SCPY	P57469 streptococ
17	88.5	8.4	619	MB14_BRAR	O57457 brachydanio
18	86.5	8.2	525	MB11_PAT	P48665 rattus norv
19	86.5	8.2	701	HRF2_XPNIA	P25980 xenopus lae
20	86.5	8.2	919	FN11_HUMAN	P18654 homo sapien
21	86.5	8.2	1231	YK13_CAEEL	Q04914 caenorhabd
22	86	8.2	405	DEMA_HUMAN	Q04913 homo sapien
23	86	8.2	416	NAP5_HUMAN	Q14513 homo sapien
24	86	8.2	611	IPAB_HUMAN	P23588 homo sapien
25	85.5	8.1	652	TPER_CHICK	P16902 gallus gall
26	85.5	8.1	5430	ACF7_HUMAN	Q94003 homo sapien
27	85	8.1	384	TNPO_GALF	P24718 galaxi cras
28	85	8.1	817	HONB_MUSDO	Q01778 musca domest
29	85	8.1	1066	T145_YEAST	P46677 saccharomyce
30	85	8.1	1205	AT51_HUMAN	P15072 homo sapien
31	84.5	8.0	559	ENL_HUMAN	Q03111 homo sapien
32	84	8.0	572	TPA2_HUMAN	O03008 drosophila
33	84	8.0	556	HIR3_HUMAN	Q96071 homo sapien

34	83.5	7.9	233	SERA_ENTHI	P21138 entamoeba h
35	83.5	7.9	597	TXP1_YEAST	P34417 saccharomyce
36	83.5	7.9	764	UBF1_HUMAN	P17480 homo sapien
37	83	7.9	369	MX_STRPY	P16946 streptococ
38	83	7.9	937	NO98_RAT	P49793 rattus norv
39	82.5	7.8	735	ADDA_RAT	O63028 rattus norv
40	82.5	7.8	1129	EC27_CAEEL	Q09228 caenorhabd
41	82	7.8	502	ATP1_TYTY	P13457 typhospha 1
42	82	7.8	554	NBL4_MOUSE	P52963 mus musculu
43	81.5	7.8	432	FTN1_MOUSE	P35821 mus musculu
44	81.5	7.8	2038	FSH_DROME	P13709 drosophila
45	81	7.7	352	SH32_MOUSE	Q62420 mus musculu

ALIGNMENTS

RESULT 1

CDNB_MOUSE STANDARD: PRT: 197 AA.

AC P46144

DT 01-NOV-1995 (rel. 32, Created)

DT 01-NOV-1995 (rel. 32, Last sequence update)

DT 15-CTN-2002 (rel. 41, Last annotation update)

DE Cyclicin-dependent kinase inhibitor 1B (Cyclicin-dependent kinase

DE inhibitor p27) (p27Kip1).

CN CDKN1B

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RK MEDLINE=94306519; PubMed=6033213;

RA Toyoshima H., Hunter T.;

RT p27, a novel inhibitor of G1 cyclin Cdk protein kinase activity, is

RL related to p21.;

RN Cell 78:67-74(1994).

RP SEQUENCE FROM N.A.

RK MEDLINE=94306518; PubMed=6033212;

RA Polyak K., Lee M.-H., Erdjument-Bromage H., Koff A., Roberts J.M.,

RT Tempst P., Massague J.;

RT "Cloning of p27Kip1, a cyclin-dependent kinase inhibitor and a

RL potential mediator of extracellular antiangiogenic signals.;"

RN Cell 78:59-66(1994).

RP INTERACTION WITH NUP50, AND MITOGENESIS.

RK MEDLINE=20271857; PubMed=10811608.

RA Mueller L., Thicke K., Huergin A., Wickham A., Eilers M.;

RT "Cyclin E-mediated elimination of p27 requires its interaction with

RL the nuclear pore-associated protein MNPAP60.;"

RN EMBO J 19:2168-2180(2000).

RP FUNCTION: Involved in G1 arrest. May mediate TOP two-induced G1

arrest. Binds to and inhibits complexes formed by cyclin E CDK2,

cyclin A/cdk2, and cyclin D/cdk4. Interaction with nucleoporin

NUP50 is required for nuclear import and for degradation of

phosphorylated p27Kip1 after mitotic re-entr.

CC SUBUNIT: Interacts with NUP50.

CC SIMILARITY: NUCLEAR.

CC -1 SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.

CC This SWISS PRO entry is copyright. It is prepared through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation

at the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement from EMBL or a request to commercial

or send an email to license@isb.scrib.ch).

EMBL: U19440; AAA21149.1; -

Query Match 91.2%; Score 958; DB 1; Length 198;
 Best Local Similarity 91.3%; Pred. No. 1, 1e-68;
 Matches 178; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MSNVRVNSGSPLEERDARQADHPKPSACRNFGPVNHEILTRILEKTRMEDEASQK 60
 1 MSNVRVNSGSPLEERDARQADHPKPSACRNFGPVNHEILTRILEKTRMEDEASQK 60
 DB 1 MSNVRVNSGSPLEERDARQADHPKPSACRNFGPVNHEILTRILEKTRMEDEASQK 60

QY 61 NEDFONHKLDEGRTEQWEGESLDEFTYRPPRPKRSACKVLAQFSQVSGKAVPLIG 120
 61 NEDFONHKLDEGRTEQWEGESLDEFTYRPPRPKRSACKVLAQFSQVSGKAVPLIG 120
 DB 61 NEDFONHKLDEGRTEQWEGESLDEFTYRPPRPKRSACKVLAQFSQVSGKAVPLIG 120

QY 121 SOANSEDPRLVQMPDSSNMGACIAGOCGMPKPRPAFRSSQNKFNATFNVSQSRN 180
 121 SOANSEDPRLVQMPDSSNMGACIAGOCGMPKPRPAFRSSQNKFNATFNVSQSRN 180
 DB 121 SOANSEDPRLVQMPDSSNMGACIAGOCGMPKPRPAFRSSQNKFNATFNVSQSRN 180

QY 181 AGVEQTPKKRPLPR 195
 181 AGVEQTPKKRPLPR 195
 DB 181 AGVEQTPKKRPLPR 195

RESULT 4
 CDBN_HUMAN STANDARD; PRT; 198 AA.
 AC P46527; Q16307;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase
 inhibitor p27) (p27kip1).
 GN CDKN1B OR KIP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catartini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-79 AND 104-152.
 RC TISSUE-Kidney;
 RX MEDLINE=94306518; PubMed=8033212;
 RA Poljak K., Lee M.-H., Erdjument-Bromage H., Koff A., Roberts J.M.,
 Tempst P., Massague J.;
 RT "Cloning of p27kip1, a cyclin dependent kinase inhibitor and a
 potential mediator of extracellular anti-tumorigenic signals.";
 RL Cell 78:59-66(1994).
 RN 12
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95188144; PubMed=7882309;
 RA Pietenpol T.A., Bohlender S.K., Sato Y., Papadopoulos N., Liu R.,
 Friedman G., Trask B.J., Roberts J.M., Kinzler K.W., Rowley J.D.;
 RT "Assignment of the human p27kip1 gene to 12p13 and its analysis in
 leukemias.";
 RL Cancer Res. 55:1206-1210(1995).
 RN 13
 RP SEQUENCE FROM N.A., AND VARIANTS TRP-15 AND GLY-109
 RA Rieder M.T., Fraum A.C., Motroya M.A., Chung M.-W., Nguyen C.F.,
 Nguyen D.A., Livingston P.J., Poel G.L., Robertson P.D.,
 Schackwitz W.S., Sherwood J.K., Wittrak L.A., Nickerson P.A.;
 RT Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
 RN 14
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 23-106 OF COMPLEX WITH CDK2
 AND CG2A.
 RX MEDLINE=96300318; PubMed=8684460;
 RA Russo A.A., Jeffrey P.D., Patten A.K., Massague J., Pavletich N.P.;
 RT "Crystal structure of the p27kip1 cyclin-dependent kinase inhibitor
 bound to the cyclin A-Cdk2 complex.";
 RL Nature 382:325-331(1996).
 CC -1- FUNCTION: Involved in G1 arrest. May mediate TGF-beta-induced G1
 arrest. Binds to and inhibits complexes formed by cyclin E-Cdk2,
 cyclin A-Cdk2, and cyclin D1-Cdk4. Interaction with nucleoprotein
 NUP50 is required for nuclear import and for degradation of
 phosphorylated p27kip1 after nuclear import (By similarity).
 CC -1- SUBUNIT: Interacts with NUP50 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES TESTED. HIGHEST
 CC LEVELS IN SKELETAL MUSCLE, LOWEST IN LIVER AND KIDNEY.
 CC -1- DOMAIN: A PEPTIDE SEQUENCE CONTAINING ONLY AA 28-79 REMAINS
 CC SUBSTANTIAL KIP1 CYCLIN A/Cdk2 INHIBITORY ACTIVITY.
 CC -1- SIMILARITY: THE N-TERMINAL OF KIP1 AND KIP ARE SIMILAR.
 CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/otm/otm.do?cmd=details/TXNIB1D10.html".
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed, changed by and/or commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announcements/>
 CC or send an email to licensing@sib.ch).

CC EMBL: Q10906; AAL29240.1; -;
 CC EMBL: S76988; AAD14244.1; -;
 CC EMBL: S76986; AAD14244.1; JOINED.
 CC EMBL: AF480891; AAL78041.1; -;
 CC PDB: 1J5U; 29-JUL-97.
 CC DR SWISS-2DPAGE: P46527; HUMAN.
 CC DR Genew: HGNC:1785; CDKN1B.
 CC DR MIM: 600778; -;
 CC DR InterPro: IPR003175; CDI.
 CC DR Pfam: PF02234; CDI; 1.
 CC DR Cell cycle: Nuclear protein; 3D structure; Polymorphism.
 CC KIP 153 159 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 CC FM TOWNT 15 15 P.S.W (IN DBSNP 2066928).
 CC FT VARIANT 15 15 /FTID-VAR_011871.
 CC FT VARIANT 109 109 V.S.S (IN DBSNP 2066927).
 CC FT /FTID-VAR_011872.
 CC FT CONF: 72 72 F.S.S (IN SPT 2).
 CC SV SEQUENCE 198 AA; 22073 MW; 111B05901C0F3FC CXC64;

Query Match 88.6%; Score 911; DB 1; Length 198;
 Best Local Similarity 87.8%; Pred. No. 1, 4e-66;
 Matches 172; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 MSNVRVNSGSPLEERDARQADHPKPSACRNFGPVNHEILTRILEKTRMEDEASQK 60
 1 MSNVRVNSGSPLEERDARQADHPKPSACRNFGPVNHEILTRILEKTRMEDEASQK 60
 DB 1 MSNVRVNSGSPLEERDARQADHPKPSACRNFGPVNHEILTRILEKTRMEDEASQK 60

QY 61 NEDFONHKLDEGRTEQWEGESLDEFTYRPPRPKRSACKVLAQFSQVSGKAVPLIG 120
 61 NEDFONHKLDEGRTEQWEGESLDEFTYRPPRPKRSACKVLAQFSQVSGKAVPLIG 120
 DB 61 NEDFONHKLDEGRTEQWEGESLDEFTYRPPRPKRSACKVLAQFSQVSGKAVPLIG 120

QY 121 SOANSEDPRLVQMPDSSNMGACIAGOCGMPKPRPAFRSSQNKFNATFNVSQSRN 180
 121 SOANSEDPRLVQMPDSSNMGACIAGOCGMPKPRPAFRSSQNKFNATFNVSQSRN 180
 DB 121 SOANSEDPRLVQMPDSSNMGACIAGOCGMPKPRPAFRSSQNKFNATFNVSQSRN 180

QY 181 AGVEQTPKKRPLPR 195
 181 AGVEQTPKKRPLPR 195
 DB 181 AGVEQTPKKRPLPR 195

RESULT 5
 CDBN_MOUSE STANDARD; PRT; 178 AA.
 AC F46529;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cyclin-dependent kinase inhibitor 1B (cyclin dependent kinase
 inhibitor p27) (p27kip1) (Fragment).
 GN CDKN1B.
 OS Mus musculus (house mouse).
 OC Eukaryota; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
 CC Marmosetta.
 OX NCBI_TaxID=9607;
 RN 11
 RP SEQUENCE FROM N.A.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: 125610; AAI16109.1;
 DR EMBL: S67368; AAB9246.1;
 DR EMBL: 009579; AAAB564.1;
 DR EMBL: 003106; AAC04313.1;
 DR EMBL: 126165; AAI19811.1;
 DR EMBL: 147233; AAB59560.1; AT-INT
 DR EMBL: AF497972; AAM1187.1;
 DR EMBL: 285996; CAP06656.1;
 DR EMBL: BC000275; AAH0275.1;
 DR EMBL: BC000312; AAH0312.1;
 DR EMBL: BC001935; AAH01935.1;
 DR EMBL: PC013967; AAI1967.1;
 DR PIR: S39357; S39357;
 DR SWISS-2DPAGE: P38936; HUMAN.
 DR Genev: HGNC:1784; CDKN1A.
 DR MIM: 116899;
 DR InterPro: IPR003175; CDI.
 DR Pfam: PF02234; CDI.1.
 DR Cell cycle, Nuclear protein, Zinc-finger, Polymorphism.
 FT ZN-FING 13 41
 FT DOMAIN 141 156
 FT VARIANT 31 31
 FT S -> R (IN DBSNP:1801270).
 FT /FTID-VAR.011870.
 SQ SEQUENCE 164 AA: 18119 MW: 980167519ALDCAG CRG64;

Query Match 15.5%, Score 163, DB 1; Length 164;
 Best Local Similarity 34.1%; Pred. No. 2,5e-06;
 Matches 42; Conservative 15; Mismatches 48; Indels 18; Gaps 3;

QY 17 DARGADHPKPS-ACRNLFGPVNHELTDLKHEKRDMEASGRKKNPFQNKPLESGYE 75
 DB 7 EVKQ--NRGSKAKRLEFVPSKLSKALDALMAGCTGFAPFRNFQVTTPLRSDFA 64
 QY 76 WQEVKSLPEFY-----RPPRPKSAKVLQESODVSGSRQAVPLIG 120
 DB 65 WEVVRGLGPKLYIPTGPRKRIELGSGPPGTSFALLGSLAEHVVLSLSCLVPSG 124
 QY 121 SQA 123
 DB 125 EQA 127

RESULT 10
 CDNL_FELCA STANDARD: PPT: 164 AA
 AC 019002;
 DT 15-DEC-1998 (rel. 37, Created)
 DT 15-DEC-1998 (rel. 37, Last sequence update)
 DT 15-DEC-1998 (rel. 37, Last annotation update)
 DE Cyclin-dependent kinase inhibitor 1 (p21) (CDK-inhibiting protein 1)
 GN CDKN1A OR CIP1 OR WAF1.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE-Lymph node;
 RX MEDLINE=98036042; PubMed=9370275;
 RA Okuda M., Minohara K., Setoguchi A., Cho K.-W., Nakamura N.,
 RA Nishigaki K., Watarai T., Cevario S., O'Brien S.J., Tsujimoto H.,
 RA Hasegawa A.;
 RT Cloning and chromosome mapping of the feline genes p21WAF1 and
 RT p27KIP1;

RL Gene 198:141-147(1997).
 CC -!- FUNCTION: MAY BE THE IMPORTANT INTERMEDIATE BY WHICH p53 MEDIATES
 CC ITS ROLE AS AN INHIBITOR OF CELLULAR CYCLINIZATION IN RESPONSE TO
 CC DNA DAMAGE. MAY BIND TO AND INHIBIT CYCLIN-DEPENDENT KINASE
 CC ACTIVITY, PREVENTING PHOSPHORYLATION OF CRITICAL CYCLIN-DEPENDENT
 CC KINASE SUBSTRATES AND BLOCKING CELL CYCLE PROGRESSION (BY
 CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: 084659; BAA23168.1;
 DR InterPro: IPR003175; CDI.
 DR Pfam: PF02234; CDI.1.
 DR Cell cycle, Nuclear protein, Zinc-finger.
 FT ZN-FING 13 41
 FT DOMAIN 141 156
 FT S -> R (IN DBSNP:1801270).
 SQ SEQUENCE 164 AA: 18315 MW: 97912A76C7BB38 CRG64;

Query Match 15.2%, Score 159.5; DB 1; Length 164;
 Best Local Similarity 27.3%; Pred. No. 4.8e-06;
 Matches 44; Conservative 23; Mismatches 71; Indels 23; Gaps 6;

QY 17 DARGADHPKPS-ACRNLFGPVNHELTDLKHEKRDMEASGRKKNPFQNKPLESGYE 76
 DB 7 EVKQ--NRGSKAKRLEFVPSKLSKALDALMAGCTGFAPFRNFQVTTPLRSDFA 65
 QY 77 WQEVKSLPEFY-----RPPRPKSAKVLQESODVSGSRQAVPLIG 129
 DB 66 EVKQ--NRGSKAKRLEFVPSKLSKALDALMAGCTGFAPFRNFQVTTPLRSDFA 114
 QY 140 ----LVDMPPSSDQNLAEGLGPKRKAALSSSSUNKR 166
 DB 115 LSCITLPHSPERPAPSPAPPTSGPRPQTSMTDFYHSKR 155

RESULT 11
 AF4_MOUSE STANDARD: PPT: 1217 AA.
 AC 088573;
 DT 16-OCT-2001 (rel. 40, Created)
 DT 16-OCT-2001 (rel. 40, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE AF-4 protein (Proto-oncogene AF4).
 GN MLT2 OR MLT2H.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sittichonidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE-Thymus;
 RA Isnard P.;
 RA Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- SIMILARITY: BELONGS TO THE AF4 FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: AF074266; AA008668.1;

Korai Initiator; Peptide

Case	Initial condition	Final condition	Time (s)	Distance (m)	Velocity (m/s)	Acceleration (m/s ²)	Force (N)	Power (W)	Energy (J)
1	0	100	10	100	10	10	10	10	10
2	0	200	20	200	20	20	20	20	20
3	0	300	30	300	30	30	30	30	30
4	0	400	40	400	40	40	40	40	40
5	0	500	50	500	50	50	50	50	50
6	0	600	60	600	60	60	60	60	60
7	0	700	70	700	70	70	70	70	70
8	0	800	80	800	80	80	80	80	80
9	0	900	90	900	90	90	90	90	90
10	0	1000	100	1000	100	100	100	100	100

[illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW mode!

Run on May 30, 2003, 08:53:57, Search time: 34 sec, Sequences (without alignments) 1181,337 Million cell updates/sec

Title: US-09-865-018b-4

Perfect score: 1051

Sequence: 1 MSNVRVNSGSPLEKRMARQ... SPNACTVQTEPKKRIKQET 197

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPREMBL_21:
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_rhiz:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1012	96.3	197	1	Q08769 ratius norv
2	1007	95.8	197	11	Q35792 ratius norv
3	928	88.3	198	4	Q96TE0 homo sapien
4	927	88.2	198	6	Q9HDC3 sus scrofa
5	925	88.0	198	4	Q9HYG6 homo sapien
6	924	87.9	198	4	Q9B0U6 homo sapien
7	740	70.4	158	4	Q43806 homo sapien
8	730	69.5	172	6	Q9BEA5 homo sapien
9	355	33.8	179	13	Q90YX4 brachydanio
10	220	20.9	210	13	Q91603 xenopus lae
11	216	20.6	42	1	Q90X60 mus musculu
12	214	20.4	335	11	Q91V06 xenopus lae
13	212	20.2	209	13	Q91V45 xenopus lae
14	190	18.1	42	4	Q90H60 homo sapien
15	182	17.3	164	11	Q64315 ratius norv
16	164	15.6	164	4	Q96LE1 homo sapien

17	162	15.4	181	4	Q14010 homo sapien
18	141.5	13.5	258	5	Q22198 caenorhabd
19	144	12.7	259	5	Q90CE5 caenorhabd
20	120.5	11.5	253	5	Q9W0P2 drosophila
21	117	11.1	184	5	Q22197 caenorhabd
22	109.5	10.4	245	5	Q94536 drosophila
23	109	10.4	255	5	P91654 drosophila
24	107.5	10.2	245	5	P91654 drosophila
25	104	9.8	259	5	Q95XW8 caenorhabd
26	103	9.8	191	10	Q04154 arabidopsis
27	103	9.7	1008	10	Q92809 arabidopsis
28	101.5	9.7	1008	10	Q92809 arabidopsis
29	95	9.1	1277	11	Q35821 arabidopsis
30	95.5	9.1	1277	11	Q35821 arabidopsis
31	95.5	9.1	570	16	Q97501 drosophila
32	95.5	9.1	630	5	Q9W433 drosophila
33	94.5	9.0	643	4	Q9NME0 homo sapien
34	94.5	9.0	1045	5	Q15852 plasmodiu
35	94.5	9.0	1211	11	Q35233 mus musculu
36	93	8.8	437	4	Q66012 homo sapien
37	93	8.8	2053	4	Q96PE2 homo sapien
38	92.5	8.8	204	5	Q97304 caenorhabd
39	92.5	8.8	204	5	Q97304 caenorhabd
40	92	8.8	303	10	Q9EYB1 arabidopsis
41	92	8.8	437	10	Q94C48 arabidopsis
42	91.5	8.7	528	4	Q95238 homo sapien
43	91.5	8.7	737	4	Q95238 homo sapien
44	91.5	8.7	738	4	Q95238 homo sapien
45	91.5	8.7	748	4	Q90B30 homo sapien

ALIGNMENTS

RESULT 1

Q08769 PRELIMINARY: PRT: 197 AA.

AC Q08769: 01-JUL-1997 (TREMBL:04, Created)

DT 01-JUL-1997 (TREMBL:04, Last sequence update)

DT 01-DEC-2001 (TREMBL:19, Last annotation update)

DE P27 K1P1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RA Kawada M., Yamagoe S., Uehara Y.;

KL Submitted (MAY 1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Kawada M., Yamagoe S., Kazuo S., Mizuno S., Uehara Y.;

KL Submitted (MAY 1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Kawada M., Yamagoe S., Murakami Y., Suzuki K., Mizuno S., Uehara Y.;

KL Submitted (MAY 1997) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Dastvan F., Reidy M.A.;

KL Submitted (MAY 1997) to the EMBL/GenBank/DBJ databases.

RA FEM1; 186824; RAAL960.1;

DR EMBL; AF015194; RAAL960.1;

DP Interpro: IPR003175; C01.

SK HSC: PF02234; C01: 1;

SC SEQUENCE 197 AA; 2239 MW; 557350780296479; 59364;

Query Match: 96.3%; Score 1012; DB 11; Length 197;

Best local similarity 96.4%; Pred. No. 197-81;

Matches 190; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

DB 61 NFDFOHKKPLEGKYEMQVEVERGSLPEFYRPPPPKSAKVVAQSDVSGSRQAVPLIG 120
 QY 121 SQANSEDRHLVDQMPOSSDQAGLAEGCAGPMMKPPAAAEISSQNKPRANPTEENVSDGSPN 189
 DB 121 SQANSEDRHLVDQKIDAEUSUGLAEGCAGTGGIKKRFALUSSQNKPRANPTEENVSDGSPN 189
 QY 181 AGTVEQTPKKPGLRRQ 196
 DB 181 SASVEQTPKKPGLRRR 196

RESULT 5

Q9NYG6 PRELIMINARY: PRT: 198 AA.

AC Q9NYG6: 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Cyclin-dependent kinase inhibitor p27kip1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEPATOMA;
 RA Li J., Wang W.-L., Yang X.-K., Yu X.-X.;
 RT Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF247551; AAF69497.1; -;
 DR InterPro: IPR003175; CDI.
 DR Pfam: PF02234; CDI; 1.
 KW kinase.
 SQ SEQUENCE 198 AA: 40675644100PFEA CRG64.
 Query Match 88.0%, Score 925; DB 4; Length 198;
 Best Local Similarity 87.2%; Pred. No. 8, 5e 74;
 Matches 171; Conservative 11; Mismatches 14; Indels 0; Gaps 0.
 QY 1 MSNVVNSGSPSLPEKMDARQADHPKPSACRNIFGVNHEELTRDLFKHCPDMEFASQPKW 60
 DB 1 MSNVVNSGSPSLPEKMDARQADHPKPSACRNIFGVNHEELTRDLFKHCPDMEFASQPKW 60
 QY 61 NFDFOHKKPLEGKYEMQVEVERGSLPEFYRPPPPKSAKVVAQSDVSGSRQAVPLIG 120
 DB 61 NFDFOHKKPLEGKYEMQVEVERGSLPEFYRPPPPKSAKVVAQSDVSGSRQAVPLIG 120
 QY 121 SQANSEDRHLVDQMPOSSDQAGLAEGCAGPMMKPPAAAEISSQNKPRANPTEENVSDGSPN 180
 DB 121 SQANSEDRHLVDQKIDAEUSUGLAEGCAGTGGIKKRFALUSSQNKPRANPTEENVSDGSPN 180
 QY 181 AGTVEQTPKKPGLRRQ 196
 DB 181 SASVEQTPKKPGLRRR 196

RESULT 6

Q9BUS6 PRELIMINARY: PRT: 198 AA.

AC Q9BUS6: 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Similar to cyclin-dependent kinase inhibitor 1b (p27, kip1).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=CERVIX;
 RA Strausberg R.;
 RT Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.

DB EMBL: BC001971; AA01971.1; -;
 DR InterPro: IPR003175; CDI.
 DR Pfam: PF02234; CDI; 1.
 KW Cyclin Kinase.
 SQ SEQUENCE 198 AA: 42041 MW: 1108499100PFEH CRG64;
 Query Match 87.9%; Score 924; DB 4; Length 198;
 Best Local Similarity 86.1%; Pred. No. 1e-73;
 Matches 171; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 1 MSNVVNSGSPSLPEKMDARQADHPKPSACRNIFGVNHEELTRDLFKHCPDMEFASQPKW 60
 DB 1 MSNVVNSGSPSLPEKMDARQADHPKPSACRNIFGVNHEELTRDLFKHCPDMEFASQPKW 60

QY 61 NFDFOHKKPLEGKYEMQVEVERGSLPEFYRPPPPKSAKVVAQSDVSGSRQAVPLIG 120
 DB 61 NFDFOHKKPLEGKYEMQVEVERGSLPEFYRPPPPKSAKVVAQSDVSGSRQAVPLIG 120

QY 121 SQANSEDRHLVDQMPOSSDQAGLAEGCAGPMMKPPAAAEISSQNKPRANPTEENVSDGSPN 180
 DB 121 SQANSEDRHLVDQKIDAEUSUGLAEGCAGTGGIKKRFALUSSQNKPRANPTEENVSDGSPN 180
 QY 181 AGTVEQTPKKPGLRRQ 196
 DB 181 SASVEQTPKKPGLRRR 196

RESULT 7

Q43806 PRELIMINARY: PRT: 158 AA.

AC Q43806: 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE p27 kip1 protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BREAST CARCINOMA;
 RA MEDLINE=9614077; PubMed=8557269;
 RA Ferrando A.A., Balbin M., Pendas A.M., Vizoso F., Velasco G.,
 RA Lopez-Otin C.;
 RT "Mutational analysis of the human cyclin-dependent kinase inhibitor
 p27 kip1 in primary breast carcinomas."
 RT Hum. Genet. 97:91-94(1996).
 DR EMBL: X84849; CAA59284.1; -;
 DR InterPro: IPR003175; CDI.
 DR Pfam: PF02234; CDI; 1.
 FT VARIANT 109 109 G -> V.
 FT NON-TER 158 158
 SQ SEQUENCE 158 AA: 17651 MW: 18627905HAZPM150 CRG64;
 Query Match 70.4%; Score 740; DB 4; Length 158;
 Best Local Similarity 86.1%; Pred. No. 1.2e-57;
 Matches 136; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 MSNVVNSGSPSLPEKMDARQADHPKPSACRNIFGVNHEELTRDLFKHCPDMEFASQPKW 60
 DB 1 MSNVVNSGSPSLPEKMDARQADHPKPSACRNIFGVNHEELTRDLFKHCPDMEFASQPKW 60

QY 61 NFDFOHKKPLEGKYEMQVEVERGSLPEFYRPPPPKSAKVVAQSDVSGSRQAVPLIG 120
 DB 61 NFDFOHKKPLEGKYEMQVEVERGSLPEFYRPPPPKSAKVVAQSDVSGSRQAVPLIG 120

QY 121 SQANSEDRHLVDQMPOSSDQAGLAEGCAGPMMKPPAAAEISSQNKPRANPTEENVSDGSPN 180
 DB 121 SQANSEDRHLVDQKIDAEUSUGLAEGCAGTGGIKKRFALUSSQNKPRANPTEENVSDGSPN 180

QY 181 AGTVEQTPKKPGLRRQ 196
 DB 181 SASVEQTPKKPGLRRR 196


```
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCBL. TISSUE=PROSTATE.
RT WATREGY D., Loda M.;
RA "Rat cyclin-dependent kinase inhibitor p27 intron";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF213701; AAF21059.1; -.
KW Kinase.
FT NON_TER
FT NON_TER
SQ SEQUENCE 42 AA; 4489 MW; 92c47c255fc3f86c GPC64.

Query Match
Best Local Similarity 20.6%; Score 216; DB 11; Length 42;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 144 LAEOCPGMRKPPAEDSSONKRRANTEENVSQSGSPNAGTVE 185
DB 1 LAEOCPGMRKPPAEDSSONKRRANTEENVSQSGSPNAGTVE 42

RESULT 12
OY1V06 PRELIMINARY: PRT; 335 AA.
AC OY1V06.
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Cyclin-dependent kinase inhibitor 1c (P57KIP2 protein) (P57)
GN CNK1C OR P57KIP2.
OS Mus musculus domesticus (western European house mouse); and
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OC NCBI_TaxID=10092; 10090;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Musculus domesticus; STRAIN=129 SV;
RX MEDLINE=20519229; PubMed=11063728;
RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt P.,
RA Lane N., Reik W., Walter J.;
RT "Sequence and functional comparison in the Beckwith-Wiedemann region;
RT implications for a novel imprinting centre and extended imprinting";
RL Hum. Mol. Genet. 9:2691-2706(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Musculus domesticus; STRAIN=129 SV;
RA Engemann S.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; STRAIN=129/SV;
RX MEDLINE=20014712; PubMed=10545601;
RA John P.M., Hodges M., Little P., Barton S.C., Surani M.A.;
RT "A human p57KIP2 transgene is not activated by passage through the
RT maternal mouse germline.";
RL Hum. Mol. Genet. 8:2211-2219(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; TISSUE=BREAST TUMOR;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases
DR EMBL: AJ276505; CAC16402.1; -.
DK EMBL: AF160139; AAF00983.1; -.
DR EMBL: BC005412; AA05412.1; -.
MGD: MGI:104564; Cdkn1c.
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1.
KM Kinase.
SQ SEQUENCE 335 AA; 35903 MW; ESC40675287FEB3F CRC64;

Query Match 20.4%; Score 214; DB 11; Length 335.
```

```
Best Local Similarity 30.0%; Pred No. 6e-11;
Matches 57; Conservative 28; Mismatches 67; Indels 38; Gaps 6;

OY 25 KLSATVNPVGVNHHETLQLKKEKMPFASGPPYNNPDPNKKPIFVGVYVPPV 92
DB 15 FSSACFSGFGVGHFFGFTFMELATNATGNNMFRNGVAVIIGPPIQWMEVDSE 74
OY 83 SLPEFYTP-----PPPKSCKVLAGEQVSGVSGVAVPLIGSQANSEIRILV 131
DB 75 SVPAFYREIVGVGCPQLQIGPPVAVV-----IPSGPPAPADGLE 120
OY 132 E--GMPSSLDVQALAEQCPMRKPPAEDSSONKRR-----ANRTEENVSGSPNAGT 183
DB 121 LAEPLGHSARASAVVAERIVRAIVASDLISDRIEVLIVALSDEIIVQANLVAI 180
OY 184 ---VEQTPKK 190
DB 181 RDGEQVPEQ 190

RESULT 13
OY1646 PRELIMINARY: PRT; 209 AA.
AC OY1646.
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE Cyclin-dependent kinase inhibitor p28.
GN Xencopus laevis (Atlantic clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97022113; PubMed=8866473;
RX Shou W., Dunphy W.G.;
RT "Cell cycle control by Xencopus p28Kix1, a developmentally regulated
RT inhibitor of cyclin-dependent kinases.";
RL Mol. Biol. Cell 7:457-469(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Shou W., Dunphy W.G.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U38644; AAC5975.1; -.
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1.
KM Kinase.
SV SEQUENCE 209 AA; 23475 MW; AEVACDA47540C6 GRC64;

Query Match 20.2%; Score 212; DB 13; Length 209;
Best Local Similarity 26.0%; Pred. No. 5e-11;
Matches 54; Conservative 39; Mismatches 73; Indels 42; Gaps 5;

OY 14 ERMDARQADHPKRS-----ACNLTGTVNHHETLQLKKEKMPFASGPPYNNPDPNKK 67
DB 10 FEMISAVAVDPKLSAGISGACNHLGPIIHGEMPSLNQLKPIQASDQDPNPPFETG 69
OY 68 KLECFYMEQVEFGSGVPEFYF-----PEFTFSACVYAGVSGVSGVAVPLIG 119
DB 70 TPLGCIQWPEPVSKIMPSPYSQNPSTIAANTIRP-----KQGPPIVSGQEP 118
OY 120 QSANSHLPHVILVMPGSSINQAGVAPVGMKPPVAAVSSQNPANPFPVNSGSP 179
DB 119 HFAPAVIVGVVFNIPDAKFNAAKIVKFGVGVGAPASANTSTGPKKFTITITVPH 178
OY 180 NAGTV-----RQTPKK 190
DB 179 KKKKILSAKPAIKAGHLDCPLDQTPKK 206

RESULT 14
OY0H60
```


PT especially breast carcinoma
 XX
 PS Disclosure: Fig 14B, 105pp; English.
 XX
 CC The present sequence represents a 27 kDa protein (p27 or Kip1) which
 CC inhibits the activation of a cyclin E-cyclin-dependent kinase2 (Cdk2)
 CC complex. A reduced relative level of kip1 is indicative of a
 CC hyperproliferative disease (particularly cancer; especially breast
 CC carcinoma) and also is prognostic for increased risk of death and/or
 CC recurrence of cancer (and may be used to determine suitable treatments).
 CC Agents that affect the activity of kip1 can be used to treat
 CC hyperproliferative conditions, e.g. to stimulate tissue or organ repair
 CC or to establish cell cultures.
 CC
 XX
 SQ Sequence 197 AA:
 Query Match 100.0%; Score 184; DB 19; Length 197;
 Best Local Similarity 100.0%; Pred. No. 7.8e-42;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DHPKPSACRNLPFPVNHPELITDLEKHCHEKMEASQKWNPFQNHKPLEGRYEWQEVER 60
 DB 22 DHPKPSACRNLPFPVNHPELITDLEKHCHEKMEASQKWNPFQNHKPLEGRYEWQEVER 81
 OY 61 GSLEPFY 67
 DB 82 GSLEPFY 88
 RESULT 4
 ID AAY08819 standard; Protein: 197 AA.
 AC AAY08819;
 XX
 DT 13-AUG-1999 (first entry)
 XX
 DE Mouse wild type p27 protein.
 XX
 KM Activation sequence; transcription factor, murine, p163, p27, treatment;
 KM binding protein; DNA binding domain; effector gene; disease; infection;
 KM tumour; leukaemia; autoimmune disease; allergy; arthritis; inflammation;
 KM transplant rejection; graft-versus-host disease; circulatory disorder;
 KM blood clot; anaemia; hormonal disorder; CNS injury.
 XX
 OS Mus sp.
 XX
 PN EP926237-A2.
 XX
 PD 30-JUN-1999.
 XX
 PF 12-DEC-1998; 98EP-0123709.
 XX
 PR 20-DEC-1997; 97DE-1056975.
 XX
 PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.
 XX
 PI Buergin A, Ellers M, Sedlacek H;
 XX
 DR WPI: 1999-349238/30.
 XX
 PT New nucleic acid construct comprising product, transcription factor
 PT gene, activation sequence and effector gene - useful for gene
 PT therapy treatment of allergies, inflammation, transplant disorders
 PT and leukaemia
 XX
 PS Disclosure: Page 49, 90pp, German.
 XX
 CC This invention describes a novel nucleic acid construct comprising the
 CC following components (a) an activation sequence for the transcription
 CC of component b, (b) component b which is constructed from component b1
 CC (a transcription factor activating domain), component b2 (murine p163
 CC or p27 binding protein) and component b3 (a transcription factor DNA

CC binding domain), (c) an activation sequence which is activated by binding
 CC of the expression product of component (b) and which induces
 CC transcription of component (d) and (d) an effector gene. The construct,
 CC preferably in a plasmid or viral vector, or cell can be used to treat a
 CC disease selected from infections, tumours, leukaemia, autoimmune
 CC diseases, allergies, arthritis, inflammations, transplant rejection,
 CC graft-versus-host disease, blood clotting disorders, circulatory
 CC disorders, anaemia, hormonal disorders and CNS injuries. This sequence
 CC represents the murine p27 protein which is used in the method of the
 CC invention.
 CC
 XX
 SQ Sequence 197 AA:
 Query Match 100.0%; Score 184; DB 20; Length 197;
 Best Local Similarity 100.0%; Pred. No. 7.8e-42;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DHPKPSACRNLPFPVNHPELITDLEKHCHEKMEASQKWNPFQNHKPLEGRYEWQEVER 60
 DB 22 DHPKPSACRNLPFPVNHPELITDLEKHCHEKMEASQKWNPFQNHKPLEGRYEWQEVER 81
 OY 61 GSLEPFY 67
 DB 82 GSLEPFY 88
 RESULT 5
 ID AAY08847 standard; Protein: 197 AA.
 AC AAY08847;
 XX
 DT 13-AUG-1999 (first entry)
 XX
 DE Murine wild type p27 protein.
 XX
 KM p163; murine; p27 inhibitor; p27-induced inhibition; cell proliferation;
 KM p27 binding domain; Ran binding domain; detection; screening; malignancy;
 KM tumour; mutant; p27 protein.
 XX
 OS Mus sp.
 XX
 PN EP926236-A1.
 XX
 PD 30-JUN-1999.
 XX
 PF 12-DEC-1998; 98EP-0123708.
 XX
 PR 20-DEC-1997; 97DE-1056975.
 XX
 PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.
 XX
 PI Buergin A, Ellers M, Sedlacek H;
 XX
 DR WPI: 1999-349237/30.
 XX
 PT New p27-inhibiting protein p163 and DNA - useful for detection
 PT and/or quantification of p163 mRNA
 XX
 PS Disclosure: Page 28, 68pp, German.
 XX
 CC This invention describes (1) a protein that inhibits p27 and thereby
 CC arrests p27-induced inhibition of cell proliferation, (2) the protein of
 CC (1) comprising at least part of the amino acid sequence of murine p163,
 CC (3) a protein that can be derived from the protein of (2) by deletion of
 CC the p27 binding domain or the Ran binding domain, (4) a protein that can
 CC be derived from the protein of (2) by deletion of all amino acid
 CC sequences other than the p27 binding domain, (5) a protein that is the
 CC human or other mammalian species homologue of a protein as in (1) (4),
 CC (6) DNA encoding the p163 protein, (7) antibodies and antibody fragments
 CC that bind to the p27 binding domain of a protein as above, (8) antibodies
 CC and antibody fragments that bind to the Ran binding domain of a protein
 CC as above, (9) antisense nucleic acids complementary to portions of the

CC following components (a) an activation sequence for the transcription
CC of component b, (b) component b which is constructed from component b1
CC (a transcription factor activating domain), component b2 (murine p163
CC or p27 binding protein) and component b3 (a transcription factor DNA
CC binding domain), (c) an activation sequence which is activated by binding
CC of the expression product of component (b) and which induces
CC transcription of component (d) and (d) an effector gene. The construct,
CC preferably in a plasmid or viral vector, or cell can be used to treat a
CC disease selected from infections, tumours, leukaemia, autoimmune
CC diseases, allergies, arthritis, inflammations, transplant rejection,
CC graft-versus-host disease, blood clotting disorders, circulatory
CC disorders, anaemia, hormonal disorders and CNS injuries. This sequence
CC represents a mutant murine p27 protein which is used to describe the
CC method of the invention.

CC Sequence 138 AA:

Query Match 98.2% Score 377; DB 20; Length 138;

Best Local Similarity 98.5% Pred. No. 4.1e-41; Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DHPKPSACRNLFGPVNHELTLDLEKHCROMEEASQKKWNPFCNNKPLEGRYEWQEVER 60

DB 7 DHPKPSACRNLFGPVNHELTLDLEKHCROMEEASQKKWNPFCNNKPLEGRYEWQEVER 66

QY 61 GSLPEFY 67

DB 67 GSLPEFY 73

RESULT 8

AA08846 ID AA08846 standard; Protein; 138 AA.

AC AA08846:

DT 13-AUG-1999 (first entry)

DE Murine mutant p27 protein from clone #850.

KM p163: murine; p27 inhibitor, p27-induced inhibition; cell proliferation;

KM p27 binding domain; Kan binding domain, detection; screening; malignancy;

KM tumour; mutant; p27 protein.

OS Mus sp.

PN EP926236-A1.

PD 30-JUN-1999.

PF 12-DEC-1998; 98EP-0123708.

PR 20-DEC-1997; 97DE-1056975.

XX (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.

PI Buerquin A, Eilers M, Sedlacek H;

DR WPI: 1999-349237/30.

XX New p27-inhibiting protein p163 and DNA - useful for detection

PT and/or quantification of p163 mRNA

XX Disclosure: Page 28; 68pp; German.

CC This invention describes (1) a protein that inhibits p27 and thereby
CC arrests p27-induced inhibition of cell proliferation, (2) the protein of
CC (1) comprising at least part of the amino acid sequence of murine p163
CC (3) a protein that can be derived from the protein of (2) by deletion of
CC the p27 binding domain or the Kan binding domain, (4) a protein that can
CC be derived from the protein of (2) by deletion of all amino acid
CC sequences other than the p27 binding domain, (5) a protein that is the
CC human or other mammalian species homologue of a protein as in (1)-(4).

CC (6) RNA encoding the p163 protein, (7) antibodies and antibody fragments
CC that bind to the p27 binding domain of a protein as above, (8) antibodies
CC and antibody fragments that bind to the Kan binding domain of a protein
CC as above, (9) antisense nucleic acids complementary to portions of the
CC RNA of (6) between codons 121 and 467, (10) a nucleic acid construct
CC coding for an antisense nucleic acid as in (9) for inhibiting the
CC proliferation of a cell, in which DNA coding for the antisense nucleic
CC acid sequence is linked to at least one activation sequence and is
CC introduced into the target cell as naked DNA or as an insert in a
CC vector of viral vector and (11) a nucleic acid construct containing the
CC RNA of (6) linked to an activation sequence that permits expression of a
CC protein as above in a cell. The RNA of (6) can be used for detection
CC and/or quantification of p163 mRNA in cells and/or tissues. Preferably by
CC Northern blotting, PCR or fluorescent in situ hybridisation. The proteins
CC can be used to produce antibodies which can be used to detect the
CC corresponding protein in cells, tissues or body fluids. The antisense
CC nucleic acids can be used to inhibit cell proliferation in vitro or in
CC vivo. The proteins can be used to screen for substances that inhibit the
CC interaction between the proteins and their natural binding partners,
CC preferably using a two hybrid system or using an affinity system in which
CC p163 or its p27-binding domain is immobilised on a solid phase, the solid
CC phase is incubated with a test substance, and the inhibition of the
CC binding of a labelled binding partner of p163 (especially p27 or Kan) is
CC measured. Assays for p163 can be used to assess the malignancy of
CC tumours. This sequence represents a mutant mouse p27 protein sequence
CC isolated from clone #826 which is used to describe the method of the
CC invention.

CC Sequence 138 AA:

Query Match 98.2% Score 377; DB 20; Length 138;

Best Local Similarity 98.5% Pred. No. 4.1e-41; Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DHPKPSACRNLFGPVNHELTLDLEKHCROMEEASQKKWNPFCNNKPLEGRYEWQEVER 60

DB 7 DHPKPSACRNLFGPVNHELTLDLEKHCROMEEASQKKWNPFCNNKPLEGRYEWQEVER 66

QY 61 GSLPEFY 67

DB 67 GSLPEFY 73

RESULT 9

AA08812 ID AA08812 standard; Protein; 183 AA.

AC AA08812:

DT 13-AUG-1999 (first entry)

DE Mouse p27 mutant protein 1.

KM Activation sequence; transcription factor; murine; p163; p27; treatment;

KM binding protein; DNA binding domain; effector gene; disease; infection;

KM tumour; leukaemia; autoimmune disease; allergy; arthritis; inflammation;

KM transplant rejection; graft-versus-host disease; circulatory disorder;

KM blood clot; anaemia; hormonal disorder; CNS injury; mutant.

OS Mus sp.

PN EP926237 A2.

PD 30-JUN-1999.

PF 12-DEC-1998; 98EP-0123709.

PI (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.

DR Buerquin A, Eilers M, Sedlacek H;

PD 30-JUN-1999.
 XX
 XX 12-DEC-1998; 98EP-0123709.
 PF
 XX 20-DEC-1997; 97DE-1056975.
 PR
 XX (HMRI) HOECHST MARION ROUSSEL DEPT GMBH.
 PA
 XX Buergin A, Eilers M, Sedlacek H;
 PI WPL; 1999-149238/30.
 DR
 XX New nucleic acid construct comprising promoter, transcription factor
 PT gene, activation sequence and effector gene - useful for gene
 PT therapy treatment of allergies, inflammation, transplant disorders
 PT and leukaemia
 PS
 XX Disclosure; Page 49; 90pp; German.
 CC This invention describes a novel nucleic acid construct comprising the
 CC following components (a) an activation sequence for the transcription
 CC of component b, (b) component b which is constructed from component b1
 CC (a transcription factor activating domain), component b2 (murine p163
 CC or p27 binding protein) and component b3 (a transcription factor DNA
 CC binding domain), (c) an activation sequence which is activated by binding
 CC of the expression product of component (b) and which induces
 CC transcription of component (d) and (d) an effector gene. The construct,
 CC preferably in a plasmid or viral vector, or cell can be used to treat a
 CC disease selected from infections, tumours, leukaemia, autoimmune
 CC diseases, allergies, arthritis, inflammations, transplant rejection,
 CC graft-versus-host disease, blood clotting disorders, circulatory
 CC disorders, anaemia, hormonal disorders and CNS injuries. This sequence
 CC represents a mutant murine p27 protein which is used to describe the
 CC method of the invention.
 XX
 XX Sequence 199 AA;
 SQ
 Query Match 98.2%; Score 377; DB 20; Length 199;
 Best Local Similarity 98.5%; Pred. No. 6,5e-41;
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DHPKPSACRNLFGPVNHELTPLDKKH-KIMPFASQPKWNFDVQNHKPIEGSPYFWQPYEP 60
 DB 18 DHPKPSACRNLFGPVNHELTPLDKKH-KIMPFASQPKWNFDVQNHKPIEGSPYFWQPYEP 77
 QY 61 GSLPEFY 67
 DB 78 GSLPEFY 84
 RESULT 12
 ID AAY08815
 AC AAY08815 standard; Protein: 199 AA.
 XX
 AC AAY08815;
 DT 13-AUG-1999 (first entry)
 DE Mouse p27 mutant protein 4.
 XX
 KM Activation sequence; transcription factor; murine; p163; p27; treatment;
 KM binding protein; DNA binding domain; effector gene; disease; infection;
 KM tumour; leukaemia; autoimmune disease; allergy; arthritis; inflammation;
 KM transplant rejection; graft-versus-host disease; circulatory disorder;
 KM blood clot; anaemia; hormonal disorder; CNS injury; mutant.
 XX
 OS Mus sp.
 XX
 PN EP926237-A2.
 XX
 PD 30-JUN-1999.
 PD
 PF 12-DEC-1998; 98EP-0123709.
 PF

XX
 PR 20-DEC-1997; 97DE-1056975.
 XX
 PA (HMRI) HOECHST MARION ROUSSEL DEPT GMBH.
 XX
 XX Buergin A, Eilers M, Sedlacek H;
 PI WPL; 1999-149238/30.
 DR
 XX New nucleic acid construct comprising promoter, transcription factor
 PT gene, activation sequence and effector gene - useful for gene
 PT therapy treatment of allergies, inflammation, transplant disorders
 PT and leukaemia
 PS
 XX Disclosure; Page 49; 90pp; German.
 CC This invention describes a novel nucleic acid construct comprising the
 CC following components (a) an activation sequence for the transcription
 CC of component b, (b) component b which is constructed from component b1
 CC (a transcription factor activating domain), component b2 (murine p163
 CC or p27 binding protein) and component b3 (a transcription factor DNA
 CC binding domain), (c) an activation sequence which is activated by binding
 CC of the expression product of component (b) and which induces
 CC transcription of component (d) and (d) an effector gene. The construct,
 CC preferably in a plasmid or viral vector, or cell can be used to treat a
 CC disease selected from infections, tumours, leukaemia, autoimmune
 CC diseases, allergies, arthritis, inflammations, transplant rejection,
 CC graft-versus-host disease, blood clotting disorders, circulatory
 CC disorders, anaemia, hormonal disorders and CNS injuries. This sequence
 CC represents a mutant murine p27 protein which is used to describe the
 CC method of the invention.
 XX
 XX Sequence 199 AA;
 SQ
 Query Match 98.2%; Score 377; DB 20; Length 199;
 Best Local Similarity 98.5%; Pred. No. 6,5e-41;
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DHPKPSACRNLFGPVNHELTPLDKKH-KIMPFASQPKWNFDVQNHKPIEGSPYFWQPYEP 60
 DB 17 DHPKPSACRNLFGPVNHELTPLDKKH-KIMPFASQPKWNFDVQNHKPIEGSPYFWQPYEP 76
 QY 61 GSLPEFY 67
 DB 77 GSLPEFY 83
 RESULT 13
 ID AAY08843
 AC AAY08843 standard; Protein: 199 AA.
 XX
 AC AAY08843;
 DT 13-AUG-1999 (first entry)
 DE Murine mutant p27 protein from clone #660.
 XX
 KM p163, murine; p27 inhibitor; p27 induced inhibition; cell proliferation;
 KM p27 binding domain; Ran binding domain; detection; screening; malignancy;
 KM tumour; mutant; p27 protein.
 XX
 OS Mus sp.
 XX
 PN EP926236-A1.
 XX
 PD 30-JUN-1999.
 PD
 PF 12-DEC-1998; 98EP-0123708.
 XX
 PP 20-DEC-1997; 97DE-1056975.
 XX
 PA (HMRI) HOECHST MARION ROUSSEL DEPT GMBH.
 XX

RESULT 15

AA08811
ID AAY08811 standard: Protein: 212 AA.

AC AAY08811:

DT 13-AUG-1999 (first entry)

DE Mouse p27 protein consensus sequence.

KW Activation sequence; transcription factor; murine; p163; p27; treatment;

KW binding protein; DNA binding domain; effector gene; disease; infection;

KW tumour; leukaemia; autoimmune disease; allergy; arthritis; inflammation;

KW transplant rejection; graft-versus-host disease; circulatory disorder;

KW blood clot; anaemia; hormonal disorder; CNS injury.

XX

OS Mus sp.

PN EP926237-A2.

PD 30-JUN-1999.

PF 12-DEC-1998; 98EP-0123709.

PR 20-DEC-1997; 97DE-1056975.

PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.

PI Buerglin A, Eilers M, Sedlacek H;

DR WPI: 1999-349238/30.

XX

PT New nucleic acid construct comprising promoter, transcription factor

PT gene, activation sequence and effector gene - useful for gene

PT therapy treatment of allergies, inflammation, transplant disorders

PT and leukaemia

XX

PS Disclosure: Page 49; 90pp; German.

XX

CC This invention describes a novel nucleic acid construct comprising the

CC following components (a) an activation sequence for the transcription

CC of component b, (b) component b which is constructed from component b1

CC (a transcription factor activating domain), component b2 (murine p163

CC or p27 binding protein) and component b3 (a transcription factor DNA

CC binding domain), (c) an activation sequence which is activated by binding

CC of the expression product of component (b) and which induces

CC transcription of component (d) and (d) an effector gene. The construct,

CC preferably in a plasmid or viral vector, or cell can be used to treat a

CC disease selected from infections, tumours, leukaemia, autoimmune

CC diseases, allergies, arthritis, inflammations, transplant rejection,

CC graft-versus-host disease, blood clotting disorders, circulatory

CC disorders, anaemia, hormonal disorders and CNS injuries. This sequence

CC represents the murine p27 protein consensus sequence which is used to

CC describe the method of the invention.

XX

SQ Sequence 212 AA:

XX

Query Match 98.2%; Score 377; DB 20; Length 212;

Best Local Similarity 98.5%; Pred. No. 7e-41;

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DHPKPSACRNLCGPVNHFLTRDLEKHRLKMFASQKKWNPQVNHKPLDSHYEWQVEVER 60

DB 18 DHPKPSACRNLCGPVNHFLTRDLEKHRLKMFASQKKWNPQVNHKPLDSHYEWQVEVER 77

OY 61 GSLPEFY 67

DB 78 GSLPEFY 84

Search completed: May 30, 2003, 08:58:26

Job time: 15.7158 secs

•

•

GenCute version 5.1.6
Copyright (c) 1993 - 2003 Computer Ltd.

OM protein - protein search, using SW model

Run on May 30, 2003, 08:55:37, Search time: 5.02067 seconds
(without alignments)
392,644 Million cell updates/sec

Title: US-09-865-018b-4_COPY_22_88

Perfect score: 384
Sequence: 1 DHPKPSACRNLEFGVNHDEL.....PLEGPTWQVFPQSLPPFY 67

Scoring table: RIGSIM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents, AA: *
1: /cgn2_6/ptodata/1/aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/aa/5A_COMB.pep.*
4: /cgn2_6/ptodata/1/aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/aa/PC10S_COMB.pep.*
6: /cgn2_6/ptodata/1/aa/Backfilest.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	384	100.0	197	US-08-275-983B-2	Sequence 2, Appl
2	384	100.0	197	US-09-240-906-B	Sequence 8, Appl
3	384	100.0	197	US-09-215-221-57	Sequence 57, Appl
4	384	100.0	197	US-08-794-002-4	Sequence 4, Appl
5	384	100.0	197	US-08-854-039B-4	Sequence 4, Appl
6	379	98.7	197	US-08-415-655-6	Sequence 6, Appl
7	377	98.2	135	US-09-215-221-56	Sequence 56, Appl
8	377	98.2	180	US-09-215-221-50	Sequence 50, Appl
9	377	98.2	193	US-09-215-221-53	Sequence 53, Appl
10	377	98.2	194	US-09-215-221-52	Sequence 52, Appl
11	377	98.2	212	US-09-215-221-55	Sequence 49, Appl
12	373	97.1	180	US-09-215-221-55	Sequence 55, Appl
13	369	96.1	177	US-09-457-568-12	Sequence 12, Appl
14	369	96.1	177	US-09-457-568-12	Sequence 12, Appl
15	369	96.1	194	US-09-215-221-51	Sequence 51, Appl
16	369	96.1	198	US-08-275-983B-3	Sequence 3, Appl
17	369	96.1	198	US-08-406-248-4	Sequence 4, Appl
18	369	96.1	198	US-08-807-333A-2	Sequence 2, Appl
19	369	96.1	198	US-09-240-906-6	Sequence 6, Appl
20	369	96.1	198	US-08-794-002-2	Sequence 2, Appl
21	369	96.1	198	US-09-457-568-26	Sequence 26, Appl
22	369	96.1	198	US-09-457-568-26	Sequence 26, Appl
23	369	96.1	334	US-09-457-568-16	Sequence 16, Appl
24	369	96.1	334	US-09-457-568-16	Sequence 16, Appl
25	369	96.1	348	US-09-457-568-14	Sequence 14, Appl
26	369	96.1	348	US-09-457-568-14	Sequence 14, Appl
27	369	96.1	365	US-09-457-568-6	Sequence 6, Appl

28	369	96.1	365	US-09-457-568-10	Sequence 10, Appl
29	369	96.1	365	US-09-457-568-10	Sequence 10, Appl
30	369	96.1	380	US-09-457-568-8	Sequence 8, Appl
31	369	96.1	380	US-09-457-568-8	Sequence 8, Appl
32	369	96.1	380	US-09-457-568-8	Sequence 8, Appl
33	369	96.1	391	US-08-568-081-2	Sequence 2, Appl
34	369	96.1	391	US-08-568-081-2	Sequence 2, Appl
35	369	96.1	391	US-09-457-568-4	Sequence 4, Appl
36	361.5	94.1	195	US-09-215-221-54	Sequence 54, Appl
37	361	94.0	198	US-08-854-039B-2	Sequence 18, Appl
38	359	93.5	80	US-09-457-568-18	Sequence 18, Appl
39	359	93.5	80	US-09-457-568-18	Sequence 18, Appl
40	359	93.5	237	US-09-457-568-20	Sequence 20, Appl
41	359	93.5	237	US-09-457-568-20	Sequence 20, Appl
42	359	93.5	252	US-09-457-568-22	Sequence 22, Appl
43	359	93.5	252	US-09-457-568-22	Sequence 22, Appl
44	356	92.7	178	US-08-794-002-6	Sequence 6, Appl
45	356	92.7	178	US-08-854-039B-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-275-983B-2
Sequence 2, Application US-08275983B
Patent No. 568665
GENERAL INFORMATION:
APPLICANT: Massague, Joan
APPLICANT: Roberts, James M.
APPLICANT: Koff, Andrew
APPLICANT: Polyak, Kornelia
TITLE OF INVENTION: Isolated p27 Protein, Nucleic Acid Molecules
NUMBER OF SEQUENCES: 19
FRESH-SEQUENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109 1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08/275,983B
FILING DATE: 13 SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US-08/174,045
FILING DATE: 07-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/COCKET NUMBER: MIT 079CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOTIF/TYP: peptide
FRAGMENT TYPE: Internal
US-08-275-983B-2
Query Match 100.0% Score 384; DB 1; Length 197;
Best Local Similarity 100.0%; Pred. No. 26-42;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
;; STREET: One Post Office Square
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02109-2170
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/854,039B
;; FILING DATE: 09-MAY-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Vincent, Matthew P.
;; REGISTRATION NUMBER: 36,709
;; REFERENCE/DOCKET NUMBER: MIV-079.04
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-832-1000
;; TELEFAX: 617-832-7000
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 197 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-854-039B-4

Query Match 100.0%; Score 184; PH 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 2,8e+42;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DHRPSACNLFQVNHHELTIDLEKRPDMEDASQPKWNPFGNHKPLEGFEYEWQVFR 60
DB 22 DHRPSACNLFQVNHHELTIDLEKRPDMEDASQPKWNPFGNHKPLEGFEYEWQVFR 61
QY 61 GSLPEFY 67
DB 82 GSLPEFY 88

RESULT 6
US-08-415-655-6
; Sequence 6, Application US/08415655
; Patent No. 6025480
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; APPLICANT: Lee, Mong-hong
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: p75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF
; TITLE OF INVENTION: SAME
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,655
; FILING DATE:
; CLASSIFICATION: 415
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678

;; REFERENCE/DOCKET NUMBER: 1747/47418
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (412) 278-0400
;; TELEFAX: (412) 391-0525
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 197 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: protein
;; HYPOTHEICAL: NO
;; ANTI-SENSE: NO
;; US-08-415-655-6

Query Match 98.7%; Score 379; PH 3; Length 197;
Best Local Similarity 98.5%; Pred. No. 1.2e+41;
Matches 66; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DHRPSACNLFQVNHHELTIDLEKRPDMEDASQPKWNPFGNHKPLEGFEYEWQVFR 60
DB 22 DHRPSACNLFQVNHHELTIDLEKRPDMEDASQPKWNPFGNHKPLEGFEYEWQVFR 61
QY 61 GSLPEFY 67
DB 82 GSLPEFY 88

RESULT 7
US-09-215-221-56
; Sequence 56, Application US/09215221
; Patent No. 6265562
; GENERAL INFORMATION:
; APPLICANT: ELLERS, MARTIN
; APPLICANT: BUEGIN, ANDREA
; APPLICANT: SEDLACKER, HANS-HARALD
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
; FILE REFERENCE: 026083/0192
; CURRENT APPLICATION NUMBER: US/09/215,221
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 197 46 975.7
; PRIOR FILING DATE: 1997-12-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 56
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: mutated p27
;; US-09-215-221-56

Query Match 98.2%; Score 377; PH 4; Length 135;
Best Local Similarity 98.5%; Pred. No. 1.4e+41;
Matches 60; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DHRPSACNLFQVNHHELTIDLEKRPDMEDASQPKWNPFGNHKPLEGFEYEWQVFR 60
DB 7 DHRPSACNLFQVNHHELTIDLEKRPDMEDASQPKWNPFGNHKPLEGFEYEWQVFR 66
QY 61 GSLPEFY 67
DB 67 GSLPEFY 73

RESULT 8
US-09-215-221-50
; Sequence 50, Application US/09215221
; Patent No. 6265562
; GENERAL INFORMATION:
; APPLICANT: ELLERS, MARTIN
; APPLICANT: BUEGIN, ANDREA

US-09-215-221-55
; Sequence 55, Application US/09215221
; Patent No. 6265562
; GENERAL INFORMATION:
; APPLICANT: EILERS, MARTIN
; APPLICANT: BUERGIN, ANDREA
; APPLICANT: SEDLACKER, HANS-HARALD
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
; FILE REFERENCE: 026083/0192
; CURRENT APPLICATION NUMBER: US/09/215,221
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 197 56 975.7
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: mutated p27
US-09-215-221-55

Query Match 97.1%; Score 373; DB 4; Length 180;
Best Local Similarity 97.0%; Pred. No. 6,66-41;
Matches 65; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DHPKPSACRNLFGPVNHFFLTPDLKFKHPRMFEASQKKNWPDQNNHPRPIEGRYWQVEVER 60
DB 7 DHPKPSACRNLFGPVNHFFLTPDLKFKHPRMFEASQKKNWPDQNNHPRPIEGRYWQVEVER 66
OY 61 GSLPEFY 67
DB 67 GSLPEFY 73

RESULT 13
US-09-457-568-12
; Sequence 12, Application US/09457568
; Patent No. 6413943
; GENERAL INFORMATION:
; APPLICANT: McArthur, James G
; APPLICANT: Gyuris, Jenio
; APPLICANT: Finer, Mitchell H
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
; TITLE OF INVENTION: Smooth Muscle Cells
; FILE REFERENCE: 106482.691
; CURRENT APPLICATION NUMBER: US/09/457,568
; CURRENT FILING DATE: 1999-12-09
; EARLIER APPLICATION NUMBER: 60/122,974
; EARLIER FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 60/163,682
; EARLIER FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-568-12

Query Match 96.1%; Score 369; DB 4; Length 177;
Best Local Similarity 94.0%; Pred. No. 2,1e-40;
Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 DHPKPSACRNLFGPVNHFFLTPDLKFKHPRMFEASQKKNWPDQNNHPRPIEGRYWQVEVER 60
DB 22 DHPKPSACRNLFGPVNHFFLTPDLKFKHPRMFEASQKKNWPDQNNHPRPIEGRYWQVEVER 81
OY 61 GSLPEFY 67
DB 82 GSLPEFY 88

RESULT 14
US-09-457-646-12
; Sequence 14, Application US/09457646
; Patent No. 6420345
; GENERAL INFORMATION:
; APPLICANT: Patel, Sallid D
; APPLICANT: McArthur, James G
; APPLICANT: Gyuris, Jenio
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
; TITLE OF INVENTION: Smooth Muscle Cells
; FILE REFERENCE: 106482.287
; CURRENT APPLICATION NUMBER: US/09/457,646
; CURRENT FILING DATE: 1999-12-09
; EARLIER APPLICATION NUMBER: 60/122,974
; EARLIER FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 60/163,682
; EARLIER FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-646-12

Query Match 96.1%; Score 369; DB 4; Length 177;
Best Local Similarity 94.0%; Pred. No. 2,1e-40;
Matches 63; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DHPKPSACRNLFGPVNHFFLTPDLKFKHPRMFEASQKKNWPDQNNHPRPIEGRYWQVEVER 60
DB 22 DHPKPSACRNLFGPVNHFFLTPDLKFKHPRMFEASQKKNWPDQNNHPRPIEGRYWQVEVER 81
OY 61 GSLPEFY 67
DB 82 GSLPEFY 88

RESULT 15
US-09-215-221-51
; Sequence 51, Application US/09215221
; Patent No. 6265562
; GENERAL INFORMATION:
; APPLICANT: EILERS, MARTIN
; APPLICANT: BUERGIN, ANDREA
; APPLICANT: SEDLACKER, HANS-HARALD
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
; FILE REFERENCE: 026083/0192
; CURRENT APPLICATION NUMBER: US/09/215,221
; CURRENT FILING DATE: 1998-12-18
; PRIOR FILING DATE: 1997-12-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: mutated p27
US-09-215-221-51

Query Match 96.1%; Score 369; DB 4; Length 194;
Best Local Similarity 95.5%; Pred. No. 2,4e-40;
Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DHPKPSACRNLFGPVNHFFLTPDLKFKHPRMFEASQKKNWPDQNNHPRPIEGRYWQVEVER 60
DB 18 DHPKPSACRNLFGPVNHFFLTPDLKFKHPRMFEASQKKNWPDQNNHPRPIEGRYWQVEVER 77

cy 61 GALLERY 67
11111
db 78 GALLERY 81

Search completed: Mon Jun 2 2003, 09:03:24
Job Name : 6_02067_0000

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compton Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2004, 04:58:12 : Search time 6.8385 Seconds
(without alignments)
991.736 Million cell updates/sec

Title: US-09-865-018b-4_COPY_22_88

Perfect score: 384
Sequence: 1 CHPKPACRNLPQVNEEL PLEGRVFWQVPEGSLPEFY 67

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 383519 seqs, 10123694 residues 383519

Total number of hits satisfying chosen parameters.

Minimum hit seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PublishedApplications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PTCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	384	100.0	197	10	US-09-865-018-4
2	369	96.1	167	8	US-08-902-572-18
3	364	94.1	194	4	US-08-902-572-18
4	369	96.1	334	8	US-08-902-572-22
5	364	96.1	348	8	US-08-902-572-24
6	369	96.1	365	8	US-08-902-572-8
7	369	96.1	480	8	US-08-902-572-6
8	369	96.1	391	8	US-08-902-572-4
9	361	94.1	194	13	US-09-865-018-2
10	359	93.5	237	8	US-08-902-572-26
11	359	93.5	252	8	US-08-902-572-28
12	356	92.7	178	10	US-09-865-018-6
13	352	91.7	70	8	US-08-902-572-20
14	147	38.3	164	9	US-08-231-268-3
15	147	38.3	164	9	US-08-231-268-5
16	147	38.3	164	10	US-09-865-018-24
17	147	38.3	164	10	US-09-940-766-2
18	144	37.5	247	10	US-09-925-297-770
19	103	26.8	191	10	US-09-733-507-2

20	103	26.8	191	10	US-09-733-507-10
21	85	22.1	137	10	US-09-733-507-14
22	83.5	21.7	212	10	US-09-733-507-12
23	73	19.0	196	10	US-09-733-507-16
24	72	18.8	208	10	US-09-733-507-13
25	71.5	18.6	176	10	US-09-733-507-11
26	71	18.5	13	10	US-09-865-018-26
27	70	18.2	190	9	US-09-923-308-4
28	66	17.2	13	10	US-09-865-018-27
29	62.5	16.3	256	9	US-09-943-308-2
30	62	16.1	932	9	US-10-072-036-137
31	62	16.1	933	9	US-10-072-036-135
32	60	15.6	282	9	US-09-845-713A-2
33	60	15.6	552	9	US-09-819-142-22
34	59.5	15.5	398	9	US-10-001-254-14
35	59.5	15.5	536	9	US-09-866-050A-185
36	54.5	15.5	540	9	US-04-866-050A-409
37	59.5	15.5	786	9	US-10-164-080-2
38	59.5	15.5	787	9	US-09-866-050A-334
39	58.5	15.2	818	10	US-09-833-435A-11
40	57	14.8	317	9	US-09-925-299-853
41	57	14.8	317	10	US-09-925-299-853
42	57	14.8	474	10	US-09-529-063-40
43	56.5	14.7	313	1	US-08-781-96A-5197
44	56.5	14.7	806	12	US-10-003-405-2
45	56.5	14.7	1038	10	US-09-908-500A-2

ALIGNMENTS

RESULT 1

US-09-865-018-4

: Sequence 4, Application US/0985018

: Patent No US20020110886A1

: GENERAL INFORMATION:

: APPLICANT: Massague, Joan

: Robertis, James M.

: Koff, Andrew

: Polyak, Kornelia

: TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHOD FOR ITS

: PRODUCTION AND USE

: NUMBER OF SEQUENCES: 27

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: FOLEY, HOAG & ELIOT LLP

: STREET: One Post Office Square

: CITY: Boston

: STATE: MA

: COUNTRY: USA

: ZIP: 02109-2170

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: PatentIn Release #1.0, Version #1.30

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/09/865,018

: FILING DATE: 24 May 2001

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US/08/854,039

: FILING DATE: 09 MAY 1997

: ATTORNEY/AGENT INFORMATION:

: NAME: Vincent, Matthew P.

: REGISTRATION NUMBER: 36,709

: REFERENCE/WORK NUMBER: MIV 079 04

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 617-832-1000

: TELEFAX: 617-832-7009

: INFORMATION FOR SEQ ID NO: 4:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 197 amino acids

: TYPE: amino acid

: TOPOLOGY: linear


```

: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-09-902-572-22

Query Match          96.1%; Score 369; DB 8; Length 334;
Best Local Similarity 94.0%; Pred. No. 3.7e-35;
Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 DHPKPSACKNFGVVDHEELITDLEKHCROMEEASQKKNWDFQNHKPLEGKYEWQEVER 60
DB 22 EHPKPSACKNFGVVDHEELITDLEKHCROMEEASQKKNWDFQNHKPLEGKYEWQEVER 81

QY 61 GSLPEFY 67
DB 82 GSLPEFY 88

RESULT 5
US-08-902-572-24
: Sequence 24, Application US/08902572
: Patent No. US20020068706A1
: GENERAL INFORMATION:
: APPLICANT: Gyuris, Jenö
: APPLICANT: Lamphere, Lou
: TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
: TITLE OF INVENTION: RELATED THERETO
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FOLEY, HOAG & ELIOT LLP
: STREET: One Post Office Square
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109-2170
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/902,572
: FILING DATE: 29-JUL-1997
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Vincent, Matthew P.
: REGISTRATION NUMBER: 36,709
: REFERENCE/DOCKET NUMBER: MIV-069.03
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-832-7000
: TELEFAX: 617-832-7000
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 348 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-902-572-24

Query Match          96.1%; Score 369; DB 8; Length 348;
Best Local Similarity 94.0%; Pred. No. 3.9e-35;
Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 DHPKPSACKNFGVVDHEELITDLEKHCROMEEASQKKNWDFQNHKPLEGKYEWQEVER 60
DB 22 EHPKPSACKNFGVVDHEELITDLEKHCROMEEASQKKNWDFQNHKPLEGKYEWQEVER 81

QY 61 GSLPEFY 67
DB 82 GSLPEFY 88

```

```

RESULT 6
US-08-902-572-8
: Sequence 8, Application US/08902572
: Patent No. US20020068706A1
: GENERAL INFORMATION:
: APPLICANT: Gyuris, Jenö
: APPLICANT: Lamphere, Lou
: TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
: TITLE OF INVENTION: RELATED THERETO
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FOLEY, HOAG & ELIOT LLP
: STREET: One Post Office Square
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109-2170
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/902,572
: FILING DATE: 29-JUL-1997
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Vincent, Matthew P.
: REGISTRATION NUMBER: 36,709
: REFERENCE/DOCKET NUMBER: MIV-069.03
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-832-7000
: TELEFAX: 617-832-7000
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 365 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-902-572-8

Query Match          96.1%; Score 369; DB 8; Length 365;
Best Local Similarity 94.0%; Pred. No. 4.1e-35;
Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 DHPKPSACKNFGVVDHEELITDLEKHCROMEEASQKKNWDFQNHKPLEGKYEWQEVER 60
DB 18 EHPKPSACKNFGVVDHEELITDLEKHCROMEEASQKKNWDFQNHKPLEGKYEWQEVER 248

QY 61 GSLPEFY 67
DB 249 GSLPEFY 255

RESULT 7
US-08-902-572-6
: Sequence 6, Application US/08902572
: Patent No. US20020068706A1
: GENERAL INFORMATION:
: APPLICANT: Gyuris, Jenö
: APPLICANT: Lamphere, Lou
: TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
: TITLE OF INVENTION: RELATED THERETO
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FOLEY, HOAG & ELIOT LLP
: STREET: One Post Office Square
: CITY: Boston
: STATE: MA

```


Query Match: 38.3%, Score 147, DB 9, Length 164;
 Best Local Similarity 42.68%, Pred. No. 1,1e-09;
 Matches 26; Conservative 11; Mismatches 24; Indels 3, Gaps 0;

QY 7 ACRNIEGPNVHFFETINDLEKHCORMEFASQPKWNEFCQNHKPIETGYEWQVFEVFGSLPEF 66
 ||| ||||| : ||| : : ||||| |||| : ||| |||
 Db 17 ACRPIFGPVDSFQISDPDTALMAGTQCAPPEWNEFVETPTLEQDFAWERVPGIGLPKI 76
 ||| ||||| : ||| : : ||||| |||| : ||| |||

QY 67 Y 67
 Db 77 Y 77

Search completed: May 30, 2003, 09:05:11
 Job time : 7.845 secs

Copyright (c) 1994 - 2003 Computer Ltd

OM protein protein search, using sw model

Run on: May 30, 2003, 08:54:42 : Search time 5.62662 Seconds
(without alignments)
1144.739 Million cell updates/sec

Title: US-09-865-018b-4_COPY_22_88

Perfect score: 384

Sequence: 1 DHPKPSACRNLFGEVNHDEL..... PLEGRYEWQFVERGSIPEFY 67

Scoring table: BLOSUM62

Gapop 10 0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 282234

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is defined by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	384	100.0	197	2 149064	cyclin-cdk inhibit
2	373	97.1	194	2 152718	gene p27Kip1 prote
3	179	46.6	316	2 G02424	cyclin-dependent k
4	173	45.1	210	2 151683	cyclin-dependent k
5	171	44.5	348	2 149262	cyclin cdk inhibit
6	154	40.1	164	2 184725	tumor suppressor p
7	147	38.3	181	2 186674	cyclin-dependent k
8	145	37.8	181	2 154380	cyclin-dependent k
9	140	36.5	154	2 149023	tumor suppressor p
10	137	35.7	143	2 A49438	p53 tumor suppress
11	115.5	30.1	258	2 T24499	hypothetical prote
12	103	26.8	191	2 T01132	cyclin-dependent k
13	87.5	23.8	184	2 T24406	hypothetical prote
14	73	19.0	146	2 T04404	hypothetical prote
15	72	18.8	195	2 H96532	hypothetical prote
16	71.5	18.6	209	2 T46140	hypothetical prote
17	69	18.0	327	2 T02707	hypothetical prote
18	69	18.0	470	2 S50083	phosphatase, short
19	65.5	17.1	246	1 S49770	hypothetical prote
20	65.5	17.1	489	2 S83401	hypothetical prote
21	65	16.9	611	1 S12566	translation initia
22	61.5	16.5	902	2 T20834	hypothetical prote
23	63	16.4	348	2 T52126	mitogen-activated
24	63	16.4	448	2 T51340	mitogen-activated
25	63	16.4	413	2 A59356	hypothetical prote
26	62	16.4	533	2 S52346	deoxyribodipyrimid
27	62.5	16.3	725	1 T18P02	gene 1 protein - p
28	62.5	16.3	496	2 T18P02	100 kDa activator
29	62.5	16.3	956	2 S64449	centromere-binding

ALIGNMENTS

RESULT 1

I49064

cyclin-cdk inhibitor p27 - mouse

N:Alternate names: Cdi p27; G1 cyclin-cyclin-dependent kinase inhibitor p27

C:Species: Mus musculus (house mouse)

C>Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 05-Nov-1999

C:Accession: I49064

R:Toyoshima, H.; Hunter, T.

Cell 78, 67-74, 1994

A:Title: p27, a novel inhibitor of G1 cyclin Cdk protein kinase activity, is related

A:Reference number: A54819; PMID:9438619; PMID:8033213

A:Accession: I49064

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-197 -RES-

A:Cross-references: EMBL:U05440; NID:553277; PIR:AAA21149.1; FID:9532772

C:Keywords: cell cycle control

Query Match 100.0% Score 384; DB 2; Length 197;

Best Local Similarity 100.0%; Pred No 1 3e-16;

Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DHPKPSACRNLFGEVNHDELTKLKHCKRMEASQKWNFDQNHKPLEGRYEWQEVER 60

DB 22 DHPKPSACRNLFGEVNHDELTKLKHCKRMEASQKWNFDQNHKPLEGRYEWQEVER 81

QY 61 GSLPEFY 67

DB 82 GSLPEFY 88

RESULT 2

I52718

gene p27Kip1 protein - human

C:Species: Homo sapiens (man)

C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000

C:Accession: I52718

R:Pietrangeli, J.A.; Reichlander, S.K.; Satoh, Y.; Papadopoulos, N.; Liu, B.; Friedman, C.

Cancer Res. 55, 1206-1210, 1995

A:Title: Assignment of the human p27Kip1 gene to 12p13 and its analysis in leukemias.

A:Reference number: 152718; PMID:85288144; PMID:7982309

A:Accession: I52718

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-198 -RES-

A:Cross-references: GB:S74988; NID:9408402; FIDN:AAH14244.1; FID:34261944

C:Genetics:

A:Gene: p27Kip1

A:Introns: 159/1

Query Match 97.1% Score 373; DB 2; Length 198;

Best Local Similarity 95.5%; Pred. No. 2.4e-35;

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: H96532
 R:Theologidis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, E.; Conway, A.B.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.I.; Jenkins, J.; Johnson-Hopwood, C.; Khoury, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.W.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: H96532
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-195 <STO>
 A:Cross-references: GB:AL000173; NID:gl0120424; P1UN-AAG1044.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F14J22.14
 A:Map position: 1

Query Match: 18.8% Score 72; DB 2; Length 195;
 Best Local Similarity 41.2%; Pred. No. 0.74;
 Matches 14; Conservative 5; Mismatches 7; Indels 8; Gaps 1;
 QY 30 DMFTASQP-----KWNFTFQNHKPLEGPEYEW 55
 Db 157 DFFSAARVEQKRFTEKYNVDVNDTLEGRYQW 190

Search completed: May 30, 2003, 09:02:44
 Job time : 6.62662 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 09:52:42 : Search time 2 sec 59 seconds
(without alignments)
972,808 Million cell updates/sec

Title: us-09-865-018b-4_copy_22_88
Perfect score: 384
Sequence: 1 DHPKPSATRNLPSPVNHETL

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	384	100.0	197	1	CDB_MOUSE
2	369	96.1	198	1	CDB_HUMAN
3	368	95.8	198	1	CDB_FELCA
4	366	95.3	198	1	CDB_CRISP
5	356	92.7	178	1	CDB_MUSVI
6	179	46.6	316	1	CDC_HUMAN
7	171	44.5	348	1	CDC_MOUSE
8	147	38.3	164	1	CDB_HUMAN
9	143	37.2	164	1	CDB_FELCA
10	140	36.5	159	1	CDB_MOUSE
11	68	17.7	532	1	PRP_POTFE
12	65.5	17.1	489	1	YN98_YEAST
13	65	16.9	611	1	IF4B_HUMAN
14	62.5	16.3	724	1	V501_HRP22
15	62.5	16.3	956	1	CR1_YEAST
16	62	16.1	670	1	K2FA_BOVIN
17	62	16.1	670	1	K2FA_HUMAN
18	62	16.1	670	1	K2FA_FALIT
19	62	16.1	686	1	K2PB_BOVIN
20	62	16.1	686	1	K2PB_HUMAN
21	62	16.1	686	1	K2PB_MOUSE
22	61.5	16.0	804	1	PRF_YEAST
23	61	15.9	450	1	INVO_LERCA
24	60	15.6	282	1	PMT_HUMAN
25	59.5	15.5	398	1	DAP3_HUMAN
26	59	15.4	261	1	YC92_RABIN
27	59	15.4	417	1	YAC1_YEAST
28	59	15.4	523	1	33H1_LYCES
29	59	15.4	805	1	SUS1_SOLTI
30	59	15.4	805	1	SUS1_LYCES
31	59	15.4	808	1	SUS1_DAUCA
32	59	15.4	2717	1	2EF1_HUMAN
33	58.5	15.2	171	1	Y501_CAPRI

RESULT 1

ID	CDB_MOUSE	STANDARD	PRT	197 AA
AC	P46414			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	15 JUN 2002 (Rel. 41, Last annotation update)			
DE	Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase inhibitor p27) (p27Kip1).			
GN	CDKN1B			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Mus;			
UX	NCBI_TaxID=10090			
RN	[1]			
PP	SEQUENCE FROM N.A.			
PP	MEDLINE=94306519; PubMed=8033213			
RA	Toyoshima H., Hunter T.			
RT	"p27, a novel inhibitor of G1 cyclin-cdk protein kinase activity, is related to p21."			
RL	Cell 78:67-74(1994).			
RN	[2]			
PP	SEQUENCE FROM N.A.			
PP	TISSUE=Embryo			
PP	MEDLINE=94306519; PubMed=8033213			
RA	Polyak K., Lee M.-H., Erdjument-Bromage H., Koff A., Roberts J.M., Tempst P., Massague J.			
RT	"Cloning of p27Kip1, a cyclin-dependent kinase inhibitor and a potential mediator of extracellular antimitogenic signals."			
RL	Cell 78:59-66(1994).			
RN	[3]			
PP	INTERACTION WITH NUP50, AND MUTAGENESIS.			
PP	STRAIN=BA1B/C			
PP	MEDLINE=20271857; PubMed=13811698			
RA	Mueller D., Thieke K., Buerger A., Dickmanns A., Eilers M.			
RT	"Cyclin E-mediated elimination of p27 requires its interaction with the nuclear pore-associated protein NUP50."			
PL	EMBO J. 19:3168-3180(2000).			
CC	... FUNCTION: Involved in G1 arrest. May mediate 1st beta-induced G1 arrest. Binds to and inhibits complexes formed by cyclin E-CDK2, cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin NUP50 is required for nuclear import and for degradation of phosphorylated p27Kip1 after nuclear import.			
CC	1- SUBUNIT: Interacts with NUP50.			
CC	1- SUBCELLULAR LOCATION: Nuclear.			
CC	1- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.			
CC	-----			
CC	This SWISS-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch)			
CC	-----			
CC	EMBL: U10440; AAA21149.1;			

023736 brassica ju
P40797 drosophila
P11325 saccharomyc
Q94911 schizosarc
P12093 oryza sativ
P34431 caenorhabdi
P76045 escherichia
P96749 corynebacte
P33294 kluyveromyc
Q24702 drosophila
P56786 arabidopsis
Q97577 homo sapien

ALIGNMENTS

34	58	15.1	514	1	GSH1_BRAJU
35	58	15.1	539	1	PNUP_DROME
36	58	15.1	894	1	SYLM_YEAST
37	58	15.1	1129	1	NRPD_SCHPO
38	58	15.1	1513	1	RPOD_ORYSA
39	58	15.1	2186	1	YL52_CABEL
40	57.5	15.0	401	1	AMP1_FALCI
41	57.5	15.0	358	1	AFOB_CORPS
42	57.5	15.0	670	1	SIP2_KLEIA
43	57.5	15.0	1557	1	IVAI_PICVI
44	57.5	15.0	2294	1	YCP2_ARATH
45	57	14.8	886	1	SNXE_HUMAN

CC -!- FUNCTION: Involved in G1 arrest. May mediate TGF-beta induced G1
 CC arrest. Binds to and inhibits complexes formed by cyclin E-CDK2,
 CC cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin
 CC NUP50 is required for nuclear import and for degradation of
 CC phosphorylated p27Kip1 after nuclear import (By similarity).
 CC -!- SUBUNIT: Interacts with NUP50 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: U84649; BAA23167.1; -
 CC InterPro: IPR003175; CDI: 1.
 CC Pfam: PF02234; CDI: 1.
 CC Cell cycle; Nuclear protein.
 CC FT DOMAIN 153 165 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 CC SEQUENCE 198 AA: 22249 MW: 54552P2146293854 CRC64;

Query Match 95.8%; Score 368; DB 1; Length 198;
 Best local Similarity 94.0%; Pred. No. 2.3e-34;
 Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 DHKPSACRNLPFGVNHHELTFLKHKCRDMEASQKWNFDQNHKPLEGKPYEWCEVER 60
 DB 22 EHPKPSACRNLPFGVNHHELTFLKHKCRDMEASQKWNFDQNHKPLEGKPYEWCEVER 81
 QY 61 GSLPEFY 67
 DB 82 GSLPEFY 88

RESULT 4

CC CDBE_CRIGR STANDARD: PRT: 198 AA.
 CC AC Q60439;
 CC DT 01-NOV-1997 (Rel. 35; Last sequence update)
 CC DT 01-NOV-1997 (Rel. 35; Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41; Last annotation update)
 CC DE Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase
 CC inhibitor p27) (p27Kip1) (p30 Kip1).
 CC GN CDKN1B OR KIP1.
 CC OS Cricetus griseus (Chinese hamster).
 CC EC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Cricetinae;
 CC Cricetus.
 CC NCBI_TaxID=10029;
 CC RN [1]
 CC SEQUENCE FROM N.A.
 CC TISSUE=Lung;
 CC MEDLINE=9471701; PubMed 930642;
 CC RA Parekh H B, Pillitteri K, Kozopoli S, Simpkins H J
 CC RT "Isolation of a hamster cDNA homologous to the mouse and human cyclin
 CC RT kinase inhibitory protein p27Kip1".
 CC RT Somat. Cell Mol. Genet. 23:147-151(1997).
 CC -!- FUNCTION: Involved in G1 arrest. May mediate TGF-beta-induced G1
 CC arrest. Binds to and inhibits complexes formed by cyclin E-CDK2,
 CC cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin
 CC NUP50 is required for nuclear import and for degradation of
 CC phosphorylated p27Kip1 after nuclear import (By similarity).
 CC -!- SUBUNIT: Interacts with NUP50 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC

CC EMBL: U49649; AAA52570.1; -
 CC InterPro: IPR003175; CDI: 1.
 CC Pfam: PF02234; CDI: 1.
 CC Cell cycle; Nuclear protein.
 CC FT DOMAIN 153 165 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 CC SEQUENCE 198 AA: 22249 MW: 243905FAF55EAGE9 CRC64;

Query Match 95.3%; Score 366; DB 1; Length 198;
 Best local Similarity 92.5%; Pred. No. 3.9e-34;
 Matches 62; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DHKPSACRNLPFGVNHHELTFLKHKCRDMEASQKWNFDQNHKPLEGKPYEWCEVER 60
 DB 22 EHPKPSACRNLPFGVNHHELTFLKHKCRDMEASQKWNFDQNHKPLEGKPYEWCEVER 81
 QY 61 GSLPEFY 67
 DB 82 GSLPEFY 88

RESULT 5

CC CDBE_MUSVI STANDARD: PRT: 178 AA
 CC AC P46529;
 CC DT 01-NOV-1995 (Rel. 42; Created)
 CC DT 01-NOV-1995 (Rel. 32; Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41; Last annotation update)
 CC DE Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase
 CC inhibitor p27) (p27Kip1) (Fragment).
 CC GN CDKN1B.
 CC OS Mus musculus (American mink).
 CC EC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
 CC Mustela.
 CC NCBI_TaxID=9667;
 CC RN [1]
 CC SEQUENCE FROM N.A.
 CC TISSUE=Lung;
 CC MEDLINE=94306518; PubMed-8033212;
 CC RA Polyak K., Lee M.-H., Erdjument-Bromage H., Koff A., Roberts J.M.,
 CC Tempst P., Massague J.;
 CC RT "Cloning of p27Kip1, a cyclin-dependent kinase inhibitor and a
 CC potential mediator of extracellular antimitogenic signals.";
 CC Cell 78:59-66(1994).
 CC RN [2]
 CC FUNCTION:
 CC MEDLINE=94115862; PubMed-8288131;
 CC RA Polyak K., Kato T.-Y., Solomon M T, Sherr C.J., Massague J.,
 CC RA Roberts J.M., Koff A.;
 CC RT "p27Kip1, a cyclin-Cdk inhibitor, links transforming growth
 CC RT factor-beta and contact inhibition to cell cycle arrest.";
 CC PI Genes Dev. 8:9-22(1994)
 CC -!- FUNCTION: Involved in G1 arrest. May mediate TGF-beta-induced G1
 CC arrest. Binds to and inhibits complexes formed by cyclin E-CDK2,
 CC cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin
 CC NUP50 is required for nuclear import and for degradation of
 CC phosphorylated p27Kip1 after nuclear import (By similarity).
 CC -!- SUBUNIT: Interacts with NUP50 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.

CC this SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC


```

RESULT 15
CB31_YEAST
ID CB31_YEAST STANDARD; PRT: 956 AA.
AC P32504;
DT 01-OCT-1993 (rel. 27, Created)
DT 01-OCT-1993 (rel. 27, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Centromere-DNA binding protein CBF3 subunit A (Kinetochores
DE protein CTF14) (Centromere-binding factor 2).
OS CBF2 OR CBF3A OR NDC10 OR CTF14 OR CBF2 OR YGR140W.
GN Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID:4932;
RN [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP MEDLINE=93252988; PubMed=8486733;
RA Jiang W., Lechner J., Carbon J.;
RT "Isolation and characterization of a gene (CBF2) specifying a protein
RT component of the budding yeast kinetochore."
RL J. Cell Biol. 121:513-519(1993).
RN [2]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP MEDLINE=93252987; PubMed=8486732;
RA Goh P.-Y., Kilmartin J.V.;
RT "NDC10: a gene involved in chromosome segregation in Saccharomyces
RT cerevisiae."
RL J. Cell Biol. 121:503-512(1993).
RN [3]
RN SEQUENCE FROM N.A.
RA van Dyck L., Skala J., de Wergifosse P., Purnelle B., Talla E.,
RA Nawrocki A., del Bino S., Goffeau A.;
EL Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: ESSENTIAL FOR CHROMOSOME SEGREGATION AND MOVEMENT OF
CC CENTROMERES ALONG MICROTUBULES. IT PLAYS A ROLE IN THE ATTACHMENT
CC OF CHROMOSOMES TO THE SPINDLE. CBF3 BINDS SELECTIVELY TO A HIGHLY
CC CONSERVED DNA SEQUENCE CALLED CDEIII, FOUND IN CENTROMERES AND IN
CC SEVERAL PROMOTERS.
CC -!- SUBUNIT: CBF3 IS FORMED OF FOUR SUBUNITS, CBF3A (CBF2), CBF3B
CC (CBF3), CBF3C (CTF13) AND CBF3D. STRONGLY INTERACTS WITH BIR1.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -----
CC This SWISS-PROT entry is Copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to licenses@isb-sib.ch).
CC -----
CC EMBL: 221627; CAA79753.1; -
CC DR EMBL: X69300; CAA49158.1; -
CC DR EMBL: 272925; CAA97153.1; -
CC DR PIR: A46432; A46432.
CC DR PIR: A46433; A46433.
CC DR SGD: S0003372; CBF2.
CC KW Nuclear protein; Chromosomal protein; DNA-binding; Centromere.
CC FT CONFLICT 774 774 K -> Q (IN REF. 1).
CC SQ SEQUENCE 956 AA; 111917 MW; C93FB/E033931E3D CRC64;
Query Match 16.3%, Score 62.5; DB 1, Length 956;
Best Local similarity 40.5%; Pred. No. 26;
Matches 17; Conservative 2; Mismatches 12; Indels 11, Gaps 2;
QY 15 VNHEELTR----DLEKHCHDMEAS-----QKKWNDFQN 45
DB 904 VNHESLDRYKAVTIPKTIQNEGFSFSLAKFLRKWRHQN 945

```

Search completed: May 30, 2003, 08:59:10
Job time : 3.85659 secs

GenCore version 5.1.6

Copyright (c) 1993 - 2003 Computer 154

OM protein - protein search, using sw model

Run on: May 30, 2003, 06:55:57, Sources: none, 11 sec, Seconds
(without alignments)
1181.337 Million cell updates/sec

Title: US-09-865-018b-4_copy_22_88

Perfect score: 384

Sequence: 1 GPRKPSA-PNLFQVNHDEL

Scoring table: PROSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 266047115 residues

Total number of hits satisfying chosen parameters: 671583

Minimum DB seq length: 0

Maximum DB seq length: 2660000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

- 1: SP_ARCHAEA*
- 2: SP_BACTERIA*
- 3: SP_FUNGI*
- 4: SP_HUMAN*
- 5: SP_INVERTEBRATE*
- 6: SP_MAMMAL*
- 7: SP_MUC*
- 8: SP_ORQUIDELLE*
- 9: SP_PHAGE*
- 10: SP_PLANT*
- 11: SP_PODENT*
- 12: SP_VIRUS*
- 13: SP_VERTERATE*
- 14: SP_UNCLASSIFIED*
- 15: SP_VIRUS*
- 16: SP_BACTERIAP*
- 17: SP_ARCHAEP*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	380	99.0	197	11	G0R769	G0R769 rattus norv
2	380	99.0	197	11	G35792	G35792 rattus norv
3	373	97.1	198	4	G96TE0	G96TE0 homo sapien
4	369	96.1	198	4	G43806	G43806 homo sapien
5	369	96.1	198	4	G9NY36	G9NY36 homo sapien
6	369	96.1	198	4	G9HUS6	G9HUS6 homo sapien
7	368	95.8	172	6	G9HEA5	G9HEA5 sus scrofa
8	368	95.8	198	6	G9HDC3	G9HDC3 sus scrofa
9	227.5	59.2	179	13	G90YX4	G90YX4 brachydanio
10	173	45.1	210	13	G91F03	G91F03 xenopus lae
11	171	44.5	335	11	G91V06	G91V06 mus musculus
12	169	44.0	209	13	G91646	G91646 xenopus lae
13	154	40.1	164	11	G64315	G64315 rattus norv
14	147	38.3	164	4	G96LEF1	G96LEF1 homo sapien
15	145	37.8	181	4	G14010	G14010 homo sapien
16	115.5	30.1	258	5	G22198	G22198 caenorhabdi

17	109	28.1	259	5	G0R6P5	G0R6P5 caenorhabdi
18	103	26.8	191	10	G04154	G04154 arabidopsis
19	103	26.8	191	10	G04154	G04154 arabidopsis
20	89.5	23.3	253	5	G0WQ02	G0WQ02 drosophila
21	88	22.9	164	10	G94V92	G94V92 nicotiana t
22	87.5	22.8	184	5	G22197	G22197 caenorhabdi
23	85	22.1	222	10	G9FKB5	G9FKB5 arabidopsis
24	84.5	21.7	192	10	G9FS28	G9FS28 fusum sativ
25	83.5	21.7	196	10	G9LJL5	G9LJL5 arabidopsis
26	82	21.4	156	10	G93YF6	G93YF6 nicotiana s
27	82	21.4	245	5	G94536	G94536 drosophila
28	82	21.4	255	5	F91654	F91654 drosophila
29	80	20.8	245	5	G91654	G91654 drosophila
30	80	20.8	246	10	G942M0	G942M0 arabidopsis
31	80	20.8	289	10	G48646	G48646 arabidopsis
32	78	20.3	189	10	G9LRY0	G9LRY0 arabidopsis
33	73	19.0	196	10	G4F597	G4F597 chenopodium
34	72	18.8	195	10	G9FX90	G9FX90 arabidopsis
35	72	18.8	195	10	G94CL9	G94CL9 arabidopsis
36	71.5	18.6	209	10	G9SCR2	G9SCR2 arabidopsis
37	71	18.5	105	5	G77670	G77670 canis famli
38	70	18.2	242	10	G9FW65	G9FW65 oryza sativ
39	70	18.2	647	5	G9VC60	G9VC60 drosophila
40	69	18.0	249	16	G9XN65	G9XN65 clostridium
41	69	18.0	470	6	G28464	G28464 monodelphis
42	67	17.4	532	5	G61133	G61133 dictyosteli
43	65.5	17.1	204	15	G9YU29	G9YU29 human immun
44	65.5	17.1	246	3	G03973	G03973 saccharomyc
45	64.5	16.8	509	2	G93F40	G93F40 shigella fl

ALIGNMENTS

RESULT 1

008769 ID: G08769 PRELIMINARY: PRT: 197 AA.
 AC: 008769;
 DT: 01-JUL-1997 (TREMBLrel. 04, Created)
 DT: 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT: 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE: P27 K1PL
 OS: Rattus norvegicus (Rat).
 OC: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC: Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX: NCBI_TaxID=10116;
 RN: [1]
 RP: SEQUENCE FROM N.A.
 RA: Kawada M., Yamagoe S., Uehara Y.;
 RL: Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN: [2]
 RP: SEQUENCE FROM N.A.
 RA: Kawada M., Yamagoe S., Kanno S., Mizuno S., Uehara Y.;
 RL: Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN: [3]
 RP: SEQUENCE FROM N.A.
 RA: Kawada M., Yamagoe S., Murakami Y., Suzuki K., Mizuno S., Uehara Y.;
 RL: Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN: [4]
 RP: SEQUENCE FROM N.A.
 RA: Castagn. F., Feisig, M.A.;
 RL: Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases
 DR: F08224, BAA19968.1, ...
 DE: EMBL: AF015194; AAB71368.1;
 DE: F08224, F0803175, CDI.
 DE: F08224, CDI, 1
 SU: SEQUENCE 197 AA; 22139 MW: 55738078C209847F CRC64;

Query Match: 99.0%; Score 380; DB 11; Length 197;
 Best Local Similarity: 98.5%; Pred. No. 6.4e-35;
 Matches: 66; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

```

QY 1 DHPKPSACRLEFVYVSHHLETRLEKPRKEMFASQKKNKFEQNKIKLEKRYEWFQVER 60
DB 1 DHPKPSACRLEFVYVSHHLETRLEKPRKEMFASQKKNKFEQNKIKLEKRYEWFQVER 60
QY 61 GSLPEFY 67
DB 62 GSLPEFY 88

RESULT 2
QY 61 GSLPEFY 67
DB 62 GSLPEFY 88

AC 043792 PRELIMINARY: PFI: 198 AA.
DI 01 JAN 1998 (FEMBLed, 05, Created)
DI 01 JAN 1998 (FEMBLed, 05, Last sequence update)
DI 01 DEC 2001 (FEMBLed, 19, Last annotation update)
DE p27.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Lox1b_10116;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN: SIKANE GAWG, TISSUE: BILDER.
RX MEDLINE 97361761; PubMed 9218722;
RA Nemer A B., Sakada Y., Fujimura K., Ohnaka S.;
E3 relation and characterization of rat p27Kip1, a cyclin dependent
R1 Kinase inhibitor *;
R2 Gene 191211-218(1997);
R3 EMBL: D63792; AAA2561.1;
R4 InterPro: IPR003175; CDI: 1;
R5 Pfam: PF02244; CDI: 1;
SQ SEQUENCE 198 AA, 22112 BW, 5574807852055162 CR64;

Query Match 99.18; Score 480; DB 11; Length 197;
Best Local Similarity 98.58; Pred. No. 6.4e 45;
Matches 66; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DHPKPSACRLEFVYVSHHLETRLEKPRKEMFASQKKNKFEQNKIKLEKRYEWFQVER 60
DB 1 DHPKPSACRLEFVYVSHHLETRLEKPRKEMFASQKKNKFEQNKIKLEKRYEWFQVER 60
QY 61 GSLPEFY 67
DB 62 GSLPEFY 88

RESULT 3
QY 61 GSLPEFY 67
DB 62 GSLPEFY 88

AC 043792 PRELIMINARY: PFI: 198 AA.
DI 01 DEC 2001 (FEMBLed, 19, Created)
DI 01 DEC 2001 (FEMBLed, 19, Last sequence update)
DI 01 MAR 2002 (FEMBLed, 20, Last annotation update)
DE CDK inhibitor p27KIP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Lox1b_9606;
RN 111
RP SEQUENCE FROM N.A.
RC MEDLINE 20372729; PubMed 1071178;
RA Millard S.S., Vidal A., Markus M., Koff A.;
E3 "A 3' UTR element in the 5' and translated region is necessary for the
R1 translation of p27 mRNA."
R2 Mol. Cell. Biol. 20:5947-5959(2000).
R3 EMBL: AY004255; AA088142.1;
R4 InterPro: IPR003175; CDI: 1;
R5 Pfam: PF02244; CDI: 1;
SQ SEQUENCE 198 AA, 22112 BW, 5574807852055162 CR64;

Query Match 97.18; Score 474; DB 4; Length 198;
Best Local Similarity 95.58; Pred. No. 4.9e 44;

```

```

QY 1 DHPKPSACRLEFVYVSHHLETRLEKPRKEMFASQKKNKFEQNKIKLEKRYEWFQVER 60
DB 1 DHPKPSACRLEFVYVSHHLETRLEKPRKEMFASQKKNKFEQNKIKLEKRYEWFQVER 60
QY 61 GSLPEFY 67
DB 62 GSLPEFY 88

RESULT 4
QY 61 GSLPEFY 67
DB 62 GSLPEFY 88

AC 043806 PRELIMINARY: PFI: 198 AA.
DI 01 JUN 1998 (FEMBLed, 06, Created)
DI 01 JUN 1998 (FEMBLed, 06, Last sequence update)
DI 01 DEC 2001 (FEMBLed, 19, Last annotation update)
DE p27 Kip1 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Lox1b_9606;
RN 111
RP SEQUENCE FROM N.A.
RC TISSUE: HEPATOMA;
RX MEDLINE 96140757; PubMed 8557269;
RA Ferrando A.A., Balbin M., Pandas A.M., Vizoso E., Velasco G.;
E3 Lapez et al. *;
R1 p27 Kip1 in primary breast carcinomas *;
R2 Hum. Genet. 97:91-94(1996);
R3 EMBL: X84849; CAA59284.1;
R4 InterPro: IPR003175; CDI: 1;
R5 Pfam: PF02244; CDI: 1;
R6 VASTANT 109 109 G - V
R7 NCBI_Lox1b_158 158
R8 SEQUENCE 158 AA, 17651 BW, 18672905842150 CR64;

Query Match 96.18; Score 469; DB 4; Length 158;
Best Local Similarity 94.08; Pred. No. 8.6e 44;
Matches 64; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 DHPKPSACRLEFVYVSHHLETRLEKPRKEMFASQKKNKFEQNKIKLEKRYEWFQVER 60
DB 1 DHPKPSACRLEFVYVSHHLETRLEKPRKEMFASQKKNKFEQNKIKLEKRYEWFQVER 60
QY 61 GSLPEFY 67
DB 62 GSLPEFY 88

RESULT 5
QY 61 GSLPEFY 67
DB 62 GSLPEFY 88

AC 043806 PRELIMINARY: PFI: 198 AA.
DI 01 OCT 2000 (FEMBLed, 15, Created)
DI 01 OCT 2000 (FEMBLed, 15, Last sequence update)
DI 01 DEC 2001 (FEMBLed, 19, Last annotation update)
DE Cyclin-dependent kinase inhibitor p27Kip1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Lox1b_9606;
RN 111
RP SEQUENCE FROM N.A.
RC TISSUE: HEPATOMA;
RA Li J., Wang W., Li Y., Yang A., Ku Y., X. X.;
E3 "Homo sapiens cyclin dependent kinase inhibitor p27Kip1 cDNA."
R1 Submitted (MAP 2000) to the EMBL/GenBank/DBJ databases.
R2 EMBL: AF247511; AA069497.1;
R3 InterPro: IPR003175; CDI: 1;

```

DR Pfam: PF02234; CDI; 1.
KW Kinase
SQ SEQUENCE 198 AA; 22099 MW; 40F7D58901C1F3FA Ch64;

Query Match
Best Local Similarity 94.0%; Score 369; DB 4; Length 198;
Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 DHPKPSACRNLFQPVNHEELTRDLKHKCRDMEASQKKNFDFONHKPLEGKRYEWEVER 60
Db 22 EHPYPSACRNLFQPVNHEELTRDLKHKCRDMEASQKKNFDFONHKPLEGKRYEWEVER 61
QY 61 GSLPEFY 67
Db 82 GSLPEFY 88
|||||

RESULT 6
Q9BUS6 PRELIMINARY; PRT; 198 AA.
ID Q9BUS6
AC Q9BUS6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-MAP-2002 (TREMBlrel. 20, Last annotation update)
DE Similar to cyclin-dependent kinase inhibitor 1b (p27, Kipl).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CERVIX;
RA Strausberg K.;
PL Submitted (JAN-2001) to the EMBL GenBank/GenBank databases
DR EMBL: B001471; AAB01471;
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1.
KW Cyclin Kinase.
SQ SEQUENCE 198 AA; 22031 MW; 1108D499160CF3ED Ch64;

Query Match
Best Local Similarity 94.0%; Score 369; DB 4; Length 198;
Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 DHPKPSACRNLFQPVNHEELTRDLKHKCRDMEASQKKNFDFONHKPLEGKRYEWEVER 60
Db 22 EHPYPSACRNLFQPVNHEELTRDLKHKCRDMEASQKKNFDFONHKPLEGKRYEWEVER 61
QY 61 GSLPEFY 67
Db 82 GSLPEFY 88
|||||

RESULT 7
Q9BEA5 PRELIMINARY; PRT; 172 AA.
ID Q9BEA5
AC Q9BEA5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE p27Kipl degradation-resistant isoform (Fragment).
GN P27KIPIR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A
RX MEDLINE=21063196; PubMed=11115398.
RA Hirano K., Hirano M., Zeng Y., Nishimura J., Hara K., Mita K.,
Nawata H., Kanai H.;
RT "Cloning and functional expression of a degradation-resistant novel
isoform of p27Kipl."

PL Biochem. J. 353:51-57(2001).
DR EMBL: AB031958; BAB39728.1; -;
DR InterPro: IPR002947; AKH.
DR Pfam: PF02234; CDI; 1.
DR PPSCITE, PS303FE, AKH, UNKNWN_1.
FT NON_TER 1 1
SQ SEQUENCE 172 AA; 13348 MW; 98EEZF3C8BC4A46E Ch64;

Query Match
Best Local Similarity 94.0%; Score 368; DB 6; Length 172;
Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 DHPKPSACRNLFQPVNHEELTRDLKHKCRDMEASQKKNFDFONHKPLEGKRYEWEVER 60
Db 14 EYKPSACRNLFQPVNHEELTRDLKHKCRDMEASQKKNFDFONHKPLEGKRYEWEVER 73
QY 61 GSLPEFY 67
Db 74 GSLPEFY 80
|||||

RESULT 8
Q9BDC3 PRELIMINARY; PRT; 198 AA.
ID Q9BDC3
AC Q9BDC3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE P27Kipl.
GN P27KIPI.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21063196; PubMed=11115398;
PA Hirano K., Hirano M., Zeng Y., Nishimura J., Hara K., Mita K.,
Nawata H., Kanai H.;
RT "Cloning and functional expression of a degradation-resistant novel
isoform of p27Kipl."
PL Biochem. J. 353:51-57(2001).
DR EMBL: AB031957; BAB39727.1; -;
DR EMBL: AB031955; BAB39725.1; -;
DR EMBL: AB031956; BAB39726.1; -;
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1.
SQ SEQUENCE 198 AA; 22201 MW; E5B01D225E5B45F Ch64;

Query Match
Best Local Similarity 94.0%; Score 368; DB 6; Length 198;
Matches 63; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 DHPKPSACRNLFQPVNHEELTRDLKHKCRDMEASQKKNFDFONHKPLEGKRYEWEVER 60
Db 22 EYKPSACRNLFQPVNHEELTRDLKHKCRDMEASQKKNFDFONHKPLEGKRYEWEVER 81
QY 61 GSLPEFY 67
Db 82 GSLPEFY 88
|||||

RESULT 9
Q90YX4 PRELIMINARY; PRT; 179 AA
ID Q90YX4
AC Q90YX4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAP-2002 (TREMBlrel. 20, Last annotation update)
DE p27-like cyclin-dependent kinase inhibitor
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


```

RA Shou W., Dunphy W.G.;
RT "Cell cycle control by Xenopus p38Fixl, a developmentally regulated
RT inhibitor of cyclin-dependent kinases";
RT Mol. Biol. Cell 7:457-469(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Shou, W. Dunphy W.G.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U38844; AAC59775.1;
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1.
KW Kinase.
SQ SEQUENCE 235 AA; 23475 MW; AEVAALAE2754Q36 CRG64;

Query Match 44.0%; Score 169; DB 13; Length 209;
Best Local Similarity 41.0%; Pred. No. 30-11;
Matches 25; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 7 ACNLPQPVNHEELTPLEKHCFDMEASQPKWNFDQNHKPLEGKYEQVFGSLPEF 66
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 30 ACNLPQPVNHEELTPLEKHCFDMEASQPKWNFDQNHKPLEGKYEQVFGSLPEF 66
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 67 Y 67
DB 90 Y 90

RESULT 13
Q64315
ID Q64315 PRELIMINARY: FRT; 164 AA.
AC Q64315;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DI 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE P21 (WAF1).
GN WAF1 OR Cipl.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95315868; PubMed=7796420;
RA el-deiry W.S., Tokino T., Waldman T., Velculescu V., Oliner J.D.,
RA Burrell M., Hill D.E., Ross J.L., Hamilton S.R., Kinzler K.W.,
RA Vogelstein B.;
RT "Topological expression of p1WAF1/Cip1 expression in normal and
RT neoplastic tissues.";
RT Cancer Res. 55:2910-2919(1995)
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=F344/N; TISSUE=LUNG;
RA Belinsky S.A.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U24174; AAC52221.1;
DR EMBL: L41275; AAC42084.1;
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1.
SQ SEQUENCE 164 AA; 16418 MW; K057P9604586445F CRG64;

Query Match 40.1%; Score 154; DB 11; Length 164;
Best Local Similarity 40.6%; Pred. No. 11e-09;
Matches 26; Conservative 11; Mismatches 27; Indels 0; Gaps 0;

QY 4 KPGACNRLFGPVNHEELTPLEKHCFDMEASQPKWNFDQNHKPLEGKYEQVFGSLPEF 63
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 13 RSKVCRPIFGPVNHEELTPLEKHCFDMEASQPKWNFDQNHKPLEGKYEQVFGSLPEF 72
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 64 PEYF 67
DB 73 PKYI 76

```

RESULT 14

```

Q96LE1
ID Q96LE1 PRELIMINARY: PRT; 164 AA.
AC Q96LE1;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DI 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Cyclin-dependent kinase inhibitor isoform.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li L.-C., Zhao H., Dahiya R.;
RT "Cloning and Characterization of p21 Isoform.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY008263; AAG15411.1;
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1.
KW Kinase.
SQ SEQUENCE 164 AA; 17827 MW; 378E002161FB3BD7 CRG64;

Query Match 38.3%; Score 147; DB 4; Length 164;
Best Local Similarity 42.6%; Pred. No. 6.8e-09;
Matches 26; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

QY 7 ACNLPQPVNHEELTPLEKHCFDMEASQPKWNFDQNHKPLEGKYEQVFGSLPEF 66
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 17 ACNLPQPVNHEELTPLEKHCFDMEASQPKWNFDQNHKPLEGKYEQVFGSLPEF 76
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 67 Y 67
DB 77 Y 77

```

RESULT 15

```

Q14010
ID Q14010 PRELIMINARY: PRT; 181 AA.
AC Q14010;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DI 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Cyclin-dependent kinase (fragment).
GN Cipl/WAF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TUMOR;
RX MEDLINE=95384154; PubMed=7655464;
RA Mousses S., Ozcelik H., Lee P.D., Malkin D., Bull S.B., Andrulis I.L.;
RT "Two variants of the Cipl/WAF1 gene occur together and are associated
RT with human cancer.";
FL Hum Mol Genet 4:1089-1092(1995)
DR EMBL: L47232; AAB59559.1;
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1.
KW Kinase.
FT NON_TER
SQ SEQUENCE 181 AA; 20083 MW; 40DA511223204F1 CRG64;

Query Match 37.2%; Score 145; DB 4; Length 181;
Best Local Similarity 42.6%; Pred. No. 1.3e-08;
Matches 26; Conservative 10; Mismatches 25; Indels 0; Gaps 0;

QY 7 ACNLPQPVNHEELTPLEKHCFDMEASQPKWNFDQNHKPLEGKYEQVFGSLPEF 66
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 34 ACNLPQPVNHEELTPLEKHCFDMEASQPKWNFDQNHKPLEGKYEQVFGSLPEF 93
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 67 Y 67

```

14: 04 Y 04

SEARCHED BY: JEFFREY M. J. JR. 2003 JUN 2 17:01
FILED BY: JEFFREY M. J. JR. 2003 JUN 2 17:01

Genome version 5.1.6
Copyright (c) 1993 - 2003. Computer Ltd

OM protein - protein search, using sw mod-1

Run on: May 30, 2003, 08:51:11 Search time 37.0754 seconds
(without alignment)
606 682 Million cell updates/sec

Title: US-09-865-018b-6

Perfect score: 952

Sequence: 1 MSNVEVSN5SPSTFEMAPQ

Scoring table: BLOSUM62

Gap 10 0 , Gapext 0.5

Search: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :			
1:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1480.DAT*		
2:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1481.DAT*		
3:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1482.DAT*		
4:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1483.DAT*		
5:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1484.DAT*		
6:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1485.DAT*		
7:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1486.DAT*		
8:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1487.DAT*		
9:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1488.DAT*		
10:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1489.DAT*		
11:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1490.DAT*		
12:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1491.DAT*		
13:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1492.DAT*		
14:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1493.DAT*		
15:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1494.DAT*		
16:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1495.DAT*		
17:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1496.DAT*		
18:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1497.DAT*		
19:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1498.DAT*		
20:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1499.DAT*		
21:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1500.DAT*		
22:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1501.DAT*		
23:	/SIUS2/gcgdata/geneseq/geneseqp-emb1/AA1502.DAT*		

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	952	100.0	178	16	AA149131 Mink kipl, p27-kipl
2	952	100.0	178	17	AA149132 Mink p27 kipl part
3	952	100.0	179	19	AA149119 Partial 27 kda pro
4	910	95.6	198	23	AA151589 Porcine p27Kipl po
5	870	91.4	194	20	AA149430 Amino acid sequenc
6	870	91.4	198	17	AA149404 Human p27 kipl. H
7	870	91.4	198	19	AA149717 27 kda protei. inh
8	870	91.4	198	19	AA146888 Amino acid sequenc
9	870	91.4	198	20	AA100768 cK1/KIP protein p2
10	870	91.4	198	21	AA1497523 Human p27 protein

11	870	91.4	198	21	AA1496052 Human cyclin depen
12	870	91.4	198	21	AA1496066 Human cyclin depen
13	870	91.4	198	21	AA144400 Human p27(Kipl) ki
14	870	91.4	198	22	AA144469 Amino acid sequenc
15	870	91.4	198	22	AA144400 Human p27 protein.
16	870	91.4	198	23	AA147880 p27-Kipl Homo sa
17	867	91.1	198	21	AA170407 Human mutant cycli
18	865	90.9	375	18	AA123534 CDK inhibitory fus
19	865	90.9	341	20	AA149094 Human p27-p16 fusi
20	865	90.9	341	21	AA1497525 Human W3 protein s
21	865	90.9	341	21	AA1496041 Antiproliferative
22	865	90.9	341	21	AA1496068 Angiogenesis inh
23	863	90.7	198	16	AA179133 Human kipl, p27-ki
24	869	90.4	365	18	AA123536 CDK inhibitory fus
25	860	90.3	365	20	AA1495107 Human p16p27 fusio
26	860	90.3	365	20	AA1495096 Human p16p27 fusio
27	860	90.3	365	21	AA1497529 Human W6 protein s
28	860	90.3	365	21	AA1496044 Antiproliferative
29	860	90.3	365	21	AA1496071 Angiogenesis inh
30	860	90.3	380	18	AA123535 CDK inhibitory fus
31	860	90.3	380	20	AA1495095 Human p16(GS)p27 f
32	860	90.3	380	21	AA1497528 Human W5 protein s
33	860	90.3	380	21	AA1496043 Antiproliferative
34	860	90.3	380	21	AA1496070 Angiogenesis inh
35	855	89.8	197	16	AA179132 Murine kipl, p27-k
36	855	89.8	197	17	AA1492708 Mouse p27 Kipl. M
37	855	89.8	197	19	AA129718 27 kda protein inh
38	855	89.8	197	20	AA1498419 Mouse wild type p2
39	855	89.8	197	20	AA1498447 Murine wild type p
40	855	89.8	197	22	AA1484650 Amino acid sequenc
41	854	89.6	365	21	AA1497527 Human W4 protein s
42	854	89.6	365	21	AA1496042 Antiproliferative
43	853	89.6	365	21	AA1496069 Angiogenesis inh
44	854	89.6	365	20	AA1496048 Mouse p27 mutant p
45	854	89.6	365	20	AA1498444 Murine mutant p27

ALIGNMENTS

RESULT 1

AA179131

AA179131 standard; protein, 178 AA.

AA179131:

27-FEB-1996 (first entry)

Mink kipl, p27 kipl or p27, cyclin E-Cdk2 activation inhibitor.

Mink kipl, p27-kipl, p27, cyclin E-Cdk2 complex, cancer,

activation inhibitor, hyperplasia, cyclin dependent kinase,

diagnosis, hyperproliferative disorder, abn. partial protein.

Mustela vison.

Key

Peptide

Location/Qualifiers

31..43

/note= "obtd. from purified kipl, and

used to design degenerate oligo-

nucleotide PCR primer"

Peptide

74..79

/note= "obtd. from purified kipl, and

used to design degenerate oligo-

nucleotide PCR primer"

Peptide

83..96

/note= "obtd. from purified kipl"

Peptide

114..122

/note= "obtd. from purified kipl"

Peptide

135..147

/note= "obtd. from purified kipl"

W09518824-A1.

XX 03 JUN 1996
XX 07 JAN 1997 940S 050724
XX 15 JUN 1994 940S 0275086
XX 07 JAN 1994 940S 0170043
XX 06 JUN 1993 N CAN 16 RES 2100 FRED
XX (SLOK) CLAVAN KETTER (N2) CAN 16 RES 2100
XX Kott A. Massaro L. Polyak K. Roberts IM
XX W111 1996 10100/111
XX N FSLDR AN116000
XX p27, an inhibitor of cyclin E/cdk2 complex activation and agents
XX which enhance and inhibit its activity, useful for treating
XX hyperproliferative and hyperproliferative disorders
XX Discovered: Fig 19a; 121pp; English
XX A partial cDNA clone (AA027014) derived from mink cells codes for
XX a 27 kDa protein, p27 Kip1 (AA027014), that is capable of binding to
XX and inhibiting the activation of a cyclin E/cdk2 complex. Mink Kip1
XX shows a high degree of homology to mouse (AA027018) and human (AA027019)
XX Kip1 proteins, and the N-terminal half of the protein shows
XX significant homology to Cip1/WAF1. Kip1 shows cell inhibitory
XX activity and prevents cdk2 activation. Overexpression inhibits
XX cell entry to the S phase. Kip1 can be produced in expression of
XX the cDNA clone in cultured cells. It can be used in vitro
XX to assay for agents that affect p27 activity, and in methods
XX for the diagnosis and treatment of hyperproliferative disorders,
XX e.g. leuko- and hyperproliferative disorders, e.g. cancer and
XX hypoplasia.
XX Sequence 178 AA:
SQ
Query Match 100.0% Score 9521 Pos 178 Length 178
Best Local Similarity 100.0% Ident. No. 4.8e 95
Matches 178 Conserved 0 Mismatches 0 Gaps 0
Q7 1 MSNVVNSNSISLEPMARQAYTKI SAKRNLEPYNHRELRKRRKRMEEASQRAW 60
DE 1 MSNVVNSNSISLEPMARQAYTKI SAKRNLEPYNHRELRKRRKRMEEASQRAW 60
Q7 61 NTFQNRHPLRKYVQWQVEKSSIFVYVQPRPRPACVQACISQVSTPQAVPLMG 120
DE 61 NTFQNRHPLRKYVQWQVEKSSIFVYVQPRPRPACVQACISQVSTPQAVPLMG 120
Q7 121 SQANSEELHVLQKIDALQALQALQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 178
DE 121 SQANSEELHVLQKIDALQALQALQVQVQVQVQVQVQVQVQVQVQVQVQV 178
AA02714
AA02714 standard: Protein: 178 AA
XX
XX AA02714
XX 27 OCT 1996 (first entry)
XX
XX Partial 27 kDa protein inhibitor of activation and cyclin E/cdk2 complex.
XX
XX Mink p27 Kip1 partial sequence
XX
XX p27 protein: Kip1, cyclin E/cdk2 cell proliferation; cancer
XX cancer hypoplasia, diagnosis, treatment; mink.
XX Mustela Sps
XX W09894121 A2
XX 06 AUG 1996
XX 05 FEB 1998 99W0 0501094
XX 05 FEB 1997 970S 0740062
XX (0072) RICHMOND CAN 16 RES 2100 FRED

XX 03 JUN 1996
XX 07 JAN 1997 940S 050724
XX 15 JUN 1994 940S 0275086
XX 07 JAN 1994 940S 0170043
XX 06 JUN 1993 N CAN 16 RES 2100 FRED
XX (SLOK) CLAVAN KETTER (N2) CAN 16 RES 2100
XX Kott A. Massaro L. Polyak K. Roberts IM
XX W111 1996 10100/111
XX N FSLDR AN116000
XX p27, an inhibitor of cyclin E/cdk2 complex activation and agents
XX which enhance and inhibit its activity, useful for treating
XX hyperproliferative and hyperproliferative disorders
XX Discovered: Fig 19a; 121pp; English
XX A partial cDNA clone (AA027014) derived from mink cells codes for
XX a 27 kDa protein, p27 Kip1 (AA027014), that is capable of binding to
XX and inhibiting the activation of a cyclin E/cdk2 complex. Mink Kip1
XX shows a high degree of homology to mouse (AA027018) and human (AA027019)
XX Kip1 proteins, and the N-terminal half of the protein shows
XX significant homology to Cip1/WAF1. Kip1 shows cell inhibitory
XX activity and prevents cdk2 activation. Overexpression inhibits
XX cell entry to the S phase. Kip1 can be produced in expression of
XX the cDNA clone in cultured cells. It can be used in vitro
XX to assay for agents that affect p27 activity, and in methods
XX for the diagnosis and treatment of hyperproliferative disorders,
XX e.g. leuko- and hyperproliferative disorders, e.g. cancer and
XX hypoplasia.
XX Sequence 178 AA:
SQ
Query Match 100.0% Score 9521 Pos 178 Length 178
Best Local Similarity 100.0% Ident. No. 4.8e 95
Matches 178 Conserved 0 Mismatches 0 Gaps 0
Q7 1 MSNVVNSNSISLEPMARQAYTKI SAKRNLEPYNHRELRKRRKRMEEASQRAW 60
DE 1 MSNVVNSNSISLEPMARQAYTKI SAKRNLEPYNHRELRKRRKRMEEASQRAW 60
Q7 61 NTFQNRHPLRKYVQWQVEKSSIFVYVQPRPRPACVQACISQVSTPQAVPLMG 120
DE 61 NTFQNRHPLRKYVQWQVEKSSIFVYVQPRPRPACVQACISQVSTPQAVPLMG 120
Q7 121 SQANSEELHVLQKIDALQALQALQVQVQVQVQVQVQVQVQVQVQVQVQV 178
DE 121 SQANSEELHVLQKIDALQALQALQVQVQVQVQVQVQVQVQVQVQVQVQV 178
AA02714
AA02714 standard: Protein: 178 AA
XX
XX AA02714
XX 27 OCT 1996 (first entry)
XX
XX Mink p27 Kip1 partial sequence
XX
XX p27 protein: Kip1, cyclin E/cdk2 cell proliferation; cancer
XX cancer hypoplasia, diagnosis, treatment; mink.
XX Mustela Sps
XX W09894121 A2
XX 06 AUG 1996
XX 05 FEB 1998 99W0 0501094
XX 05 FEB 1997 970S 0740062
XX (0072) RICHMOND CAN 16 RES 2100 FRED

XX Porter PL; Roberts JM;
 XX WPI: 1998-437612/37.
 DR N-PSDB: AAV47519.
 XX Assays for protein p27 inhibiting activation of cyclin E-Cdk2
 PT complex - useful for, e.g. diagnosis and prognosis of cancer,
 PT especially breast carcinoma
 XX Disclosure: Fig 13B; 105pp; English.
 XX The present sequence represents a partial 27 kDa protein (p27 or Kip1)
 CC which inhibits the activation of a cyclin E-cyclin-dependent kinase2
 CC (Cdk2) complex. A reduced relative level of Kip1 is indicative of a
 CC hyperproliferative disease (particularly cancer, especially breast
 CC carcinoma) and also is prognostic for increased risk of death and/or
 CC recurrence of cancer (and may be used to determine suitable treatments).
 CC Agents that affect the activity of Kip1 can be used to treat
 CC hyperproliferative conditions, e.g. to stimulate tissue or organ repair
 CC or to establish cell cultures.
 XX Sequence 178 AA;

Query Match 103.3%; Score 952; DB 19; Length 178;
 Best Local Similarity 100.0%; Pred. No. 3.8e-95;
 Matches 178; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MSNVVSNVSGPSLERMDARAEYKPKPSACPNLFSPVNHRELTPDLKHPDMEASQKWK 60
 DB 1 MSNVVSNVSGPSLERMDARAEYKPKPSACPNLFSPVNHRELTPDLKHPDMEASQKWK 60
 QY 61 NFDQNHKPLEGKYEWEVEKSGSLPFFYYPPPPKCAKVPAGFSGVSSSTPQAVPLMG 120
 DB 61 NFDQNHKPLEGKYEWEVEKSGSLPFFYYPPPPKCAKVPAGFSGVSSSTPQAVPLMG 120
 QY 121 SCANSEDLHLVDQKIDTADNAGLAEOCTGIRKRPATDDSSPQNKRRNTEENVSDGS 178
 DB 121 SCANSEDLHLVDQKIDTADNAGLAEOCTGIRKRPATDDSSPQNKRRNTEENVSDGS 178

RESULT 4
 AAM51589
 ID AAM51589 standard; Protein: 198 AA.
 AC AAM51589;

XX 01-FEB-2002 (first entry)
 XX Porcine p27Kip1 polypeptide #2.

XX Fig: antiarteriosclerosis; cytostatic; gene therapy; p27Kip1;
 KW proteasome decomposition resistance; cancer; arteriosclerosis.

XX Sus scrofa.

XX JP2001258561-A.

XX 25 SEP-2001.

XX 17-MAR-2000; 2000JP-0076840.

XX 17-MAR-2000; 2000JP-0076840.

XX (UYKY-) UNIV KYUSHU.

XX WPI: 2002-003329/01

XX N-PSDB: ABA01080.

XX Nucleic acid and amino acid sequence for showing resistance against
 PT proteasome decomposition, comprises a new p27Kip1 molecular species -

XX Disclosure: Page 8-9; 12pp; Japanese.

XX The invention relates to a novel p27Kip1 polynucleotide and protein
 CC The p27Kip1 protein shows resistance to proteasome decomposition
 CC and can be used in the treatment of cancers and arteriosclerosis. The
 CC invention also relates to a recombinant vector containing the
 CC polynucleotide, and to a transformant containing the recombinant
 CC vector. The present sequence is a p27Kip1 polypeptide.
 XX Sequence 198 AA;

Query Match 95.6%; Score 910; DB 23; Length 198;
 Best Local Similarity 95.5%; Pred. No. 1.1e-90;
 Matches 170; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MSNVVSNVSGPSLERMDARAEYKPKPSACPNLFSPVNHRELTPDLKHPDMEASQKWK 60
 DB 1 MSNVVSNVSGPSLERMDARAEYKPKPSACPNLFSPVNHRELTPDLKHPDMEASQKWK 60
 QY 61 NFDQNHKPLEGKYEWEVEKSGSLPFFYYPPPPKCAKVPAGFSGVSSSTPQAVPLMG 120
 DB 61 NFDQNHKPLEGKYEWEVEKSGSLPFFYYPPPPKCAKVPAGFSGVSSSTPQAVPLMG 120
 QY 121 SCANSEDLHLVDQKIDTADNAGLAEOCTGIRKRPATDDSSPQNKRRNTEENVSDGS 178
 DB 121 SCANSEDLHLVDQKIDTADNAGLAEOCTGIRKRPATDDSSPQNKRRNTEENVSDGS 178

RESULT 5
 AAW94930
 ID AAW94930 standard; Protein: 194 AA.

XX AAW94930;

XX 11-MAY-1999 (first entry)

XX Amino acid sequence of p27 protein.

XX Vascular proliferative disease; p27 protein; fusion protein; restenosis;
 KW arteriosclerosis; angiogenesis; smooth muscle; cell proliferation; TK;
 KW thymidine kinase; gancyclovir; GCV.

XX Homo sapiens.

XX WO9903508-A2.

XX 28-JAN-1999.

XX 21 JUL-1998; 98WO US15025.

XX 21-JUL-1997; 97US-0897333.

XX (UNMI) UNIV MICHIGAN.

XX Nabel EG, Nabel GJ;

XX WPI: 1999-131876/11.

XX N-PSDB: AAX17752.

XX Treating vascular proliferative disease with p27 gene - used
 PT particularly to treat restenosis, arteriosclerosis and angiogenesis
 PT or to inhibit intimal smooth muscle cell growth

XX Example 1; Fig 5; 40pp; English.

XX The invention relates to a method of treating vascular proliferative
 CC diseases. The method comprises in vivo administration of a gene encoding
 CC p27; or fusion proteins consisting of p27 linked to a second polypeptide.
 CC p27 is used to treat, or prevent, restenosis (coronary or peripheral),
 CC arteriosclerosis or angiogenesis, or generally to inhibit growth of
 CC intimal smooth muscle cells. The method is based on the discovery that
 CC p27 functions in arteries to control response to acute injury and cell
 CC proliferation. Its (over)expression is sufficient to inhibit growth of
 CC vascular smooth muscle cells in vivo. Arresting cells with p27 renders

Matches 162; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSNVAVSNGSPSIFMIFARQARYPRPSACRNIFGVNHEELIFELFKHFSMELASQPKW 60
 DB 1 MSNVAVSNGSPSIFMIFARQARYPRPSACRNIFGVNHEELIFELFKHFSMELASQPKW 60
 QY 61 NFEQGNHKKPLEKRYEWVEVEKSLPEFYYPKPPKPKACVPAQESQVSGTQCAVPLMG 120
 DB 61 NFEQGNHKKPLEKRYEWVEVEKSLPEFYYPKPPKPKACVPAQESQVSGTQCAVPLMG 120
 QY 121 SQANSEDLHLVDQKTDIAWAGLABQCTGIRKRPATDSSQNKRNKRNTEENVSDGS 178
 DB 121 APANSEDLHLVDKIDFSQSGTGLAEQCAQIRKPPATDSSQNKRNKRNTEENVSDGS 178

RESULT 8

AAW46888 standard; Protein: 198 AA.

XX AC AAW46888;

XX DT 15 JUN 1998 (first entry)

XX DE Amino acid sequence of the p27KIP1 protein.

XX KW E7 oncoprotein; proliferative state; HPV; kinase activity;

XX KW cyclin/cyclin-dependent kinase; p21CIP1; interaction; inactivation;

XX KW cyclin/cyclin-dependent kinase inhibitor.

XX OS Homo sapiens.

XX PN US5736318-A.

XX PD 07-APR-1998.

XX PF 17-MAR-1995; 95US-0406248.

XX PR 17-MAR-1995; 95US-0406248.

XX PA (HARD) HARVARD COLLEGE.

XX PA (HARD) UNIV HARVARD.

XX PI Jones DL, Munger K;

XX PI WPI: 1998-239202/21.

XX DR N-PSDB; AAV16719.

XX PT Evaluation of proliferative state of cells transformed with human
 PT papilloma virus - by determining cyclin-dependent kinase activity
 PT induced by E7 onco-protein

XX PS Disclosure; Columns 17-18; 14pp; English.

XX CC The present sequence represents a p27KIP1 protein, which is part of a
 CC family of small cyclic-dependent kinase inhibitors. The proliferative
 CC state of a cell transformed with human papillomavirus (HPV) can be
 CC evaluated in the following manner. Cyclin/cyclin dependent kinase
 CC complexes containing protein p27KIP1 are isolated from the transformed
 CC cell, and the HPV E7 oncoprotein (AAW46888) added to the isolated
 CC protein. Cyclin/cyclin-dependent kinase complexes are isolated from an
 CC untransformed cell that is substantially homogenic with the transformed
 CC cell, and the HPV E7 oncoprotein added. The kinase activities of the 2
 CC samples are measured, where a proliferating transformed cell has a
 CC greater kinase activity than the untransformed cell. The method is
 CC used for determining the extent of interaction and/or inactivation
 CC between a cyclin/cyclin-dependent kinase inhibitor and the HPV E7
 CC oncoprotein and thus evaluating the proliferative state of a transformed
 CC cell.

XX SQ Sequence 198 AA;

Query Match

Best Local Similarity 91.4%; Score 870; DB 19; Length 198;

Pred No. 3 6e-86;

Matches 162; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSNVAVSNGSPSIFMIFARQARYPRPSACRNIFGVNHEELIFELFKHFSMELASQPKW 60
 DB 1 MSNVAVSNGSPSIFMIFARQARYPRPSACRNIFGVNHEELIFELFKHFSMELASQPKW 60
 QY 61 NFEQGNHKKPLEKRYEWVEVEKSLPEFYYPKPPKPKACVPAQESQVSGTQCAVPLMG 120
 DB 61 NFEQGNHKKPLEKRYEWVEVEKSLPEFYYPKPPKPKACVPAQESQVSGTQCAVPLMG 120
 QY 121 SQANSEDLHLVDQKTDIAWAGLABQCTGIRKRPATDSSQNKRNKRNTEENVSDGS 178
 DB 121 APANSEDLHLVDKIDFSQSGTGLAEQCAQIRKPPATDSSQNKRNKRNTEENVSDGS 178

RESULT 9

AAW00768 standard; Protein: 198 AA.

XX AC AAY00768;

XX DT 14-MAY-1999 (first entry)

XX DE CKI/KIP protein p27.

XX KW CKI/KIP protein; p27 protein; cyclin kinase inhibitor; cancer;

XX KW hyperproliferative disorder.

XX OS Homo sapiens.

XX PN WO9904238-A2.

XX PD 28-JAN-1999.

XX PF 14-JUL-1998; 98WO-US14566.

XX PR 15-JUL-1997; 97US-0893276.

XX XX (DEAC-) DEACONESS HOSPITAL.

XX PA (MITO-) MITOTIX INC.

XX PI Draetta G, Loda M, Pagano M, Rolfe M;

XX PI WPI: 1999-132426/11

XX DR N-PSDB; AAX21817.

XX PT Methods for diagnosis and prognosis of hyperproliferative disorders
 PT - by determining the level of cyclin kinase inhibitor protein(s),
 PT particularly p27

XX PS Claim 18; Page 36 37; 53pp; English.

XX CC This sequence is the cyclin kinase inhibitor (CKI) protein p27. The
 CC invention relates to a method for diagnosing a hyperproliferative
 CC disorder, associated with the destabilization of a CKI protein in cells
 CC of a patient, comprises: (i) ascertaining the CKI protein level in a
 CC sample of patient cells; and (ii) diagnosing the presence or absence of a
 CC hyperproliferative disorder by utilizing the ascertained CKI protein
 CC level, where a reduced CKI protein level, relative to a normal control
 CC cell sample, correlates with the presence of a hyperproliferative
 CC disorder. The methods are useful for diagnosing disorders associated with
 CC hyperproliferation, evaluating their aggressiveness and/or rate of
 CC recurrence and as prognosis for evaluating a cancer patient's risk of
 CC death from the observations. Treatment can be applied on the basis of
 CC the patient's risk of death and/or recurrence of the cancer. The
 CC diagnostic methods may also be employed as follow-up to treatment,
 CC e.g. quantitation of the level of p27 protein may be indicative of the
 CC effectiveness of current or previously employed cancer therapies as well
 CC as the effect of these therapies upon patient prognosis. The methods and
 CC reagents allow the detection of loss of p27 protein from a cell in order
 CC to diagnose and phenotype proliferative disorders arising from
 CC tumorigenic transformation of cells, or other hyperplastic or neoplastic
 CC transformation processes as well as differentiative disorders such as

The present sequence is that of human p27, a cyclin dependent kinase inhibitor (CKI) that inhibits smooth muscle cell proliferation. A claimed method for inhibiting smooth muscle cell hyperproliferation involves transducing smooth muscle cells with a replication-deficient recombinant adenovirus that lacks a functional E1 region and a functional E4 region, and comprises a transgene encoding a CDK1. The CDK1 is selected from an INK4 family protein such as human p16, a CIP/KIP family protein such as p27, active fragments of these, or fusion proteins comprising (active fragments of) an INK4 family protein and a CIP/KIP family protein (see AAY96046 and AAY96049). The method is used to inhibit mammalian smooth muscle cell hyperproliferation induced by injury caused by angioplasty, stent placement or vein grafting. It is useful for treating vascular pathologies, e.g. restenosis. Also claimed are recombinant lentiviruses encoding CDK1s.

XX Sequence 198 AA:

XX Query Match 91.4% Score 870, BB 21, Length 198,

XX Best Local Similarity 91.0% Pred No 3,6e-86)

XX Matches 162, conservative 7, Mismatches 9, Indels 0, Gaps 0;

QY 1 MSNVVSYNGSFSILRMCAEACYPKPSACFNIFGVNHEELTPLEKHEFTMEFASQPKW 60

DB : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1 MSNVVSYNGSFSILRMCAEACYPKPSACFNIFGVNHEELTPLEKHEFTMEFASQPKW 60

DB : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 NFDQNHKFLCKYKMGCFVKYSIIFFVYFPPPKGACKYFAVESGTSFGAVFLMG 120

DB : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 NFDQNHKFLCKYKMGCFVKYSIIFFVYFPPPKGACKYFAVESGTSFGAVFLMG 120

DB : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 SQANSEDTHLVDQFDTADNQLALAEQCTGKTKKPTATENSSFNKKPANKRFPENVSDGS 178

DB : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 APANSEDTHLVDKTPDSVSTGLAEQAGIKKKPAHLCSSSTLNKKPANKRFTENVSDGS 178

DB : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12

AAY96066

ID ID AAY96066 standard; Protein: 198 AA.

XX AC AAY96066:

XX 05-DEC-2000 (first entry)

XX Human cyclin dependent kinase inhibitor p27.

DE Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; human; p27;

XX angiogenesis inhibitor; neoplasia; rheumatoid arthritis;

KW endometriosis; psoriasis; vascular retinopathy; cytostatic;

KW antiarthritic; antihematuric; gynecological; antipsoriatic;

KW antiproliferative; gene therapy.

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FF Domain 25..93

FT Domain /note= "CDK inhibitory domain"

FT Domain 144..194

FT Peptide /note= "QT domain"

FT Peptide 152..166

FT Peptide /note= "nuclear localisation signal"

FT Modified-site 10..14

FT /note= "n-phosphorylated; weak CDK phosphorylation site"

FT Modified-site 178..181

FT /note= "n-phosphorylated; phosphorylation site for proline-directed kinases"

FT Modified-site 187..190

FT /note= "n-phosphorylated; CDF phosphorylation consensus site"

XX

XX W0200052158 A1.

XX

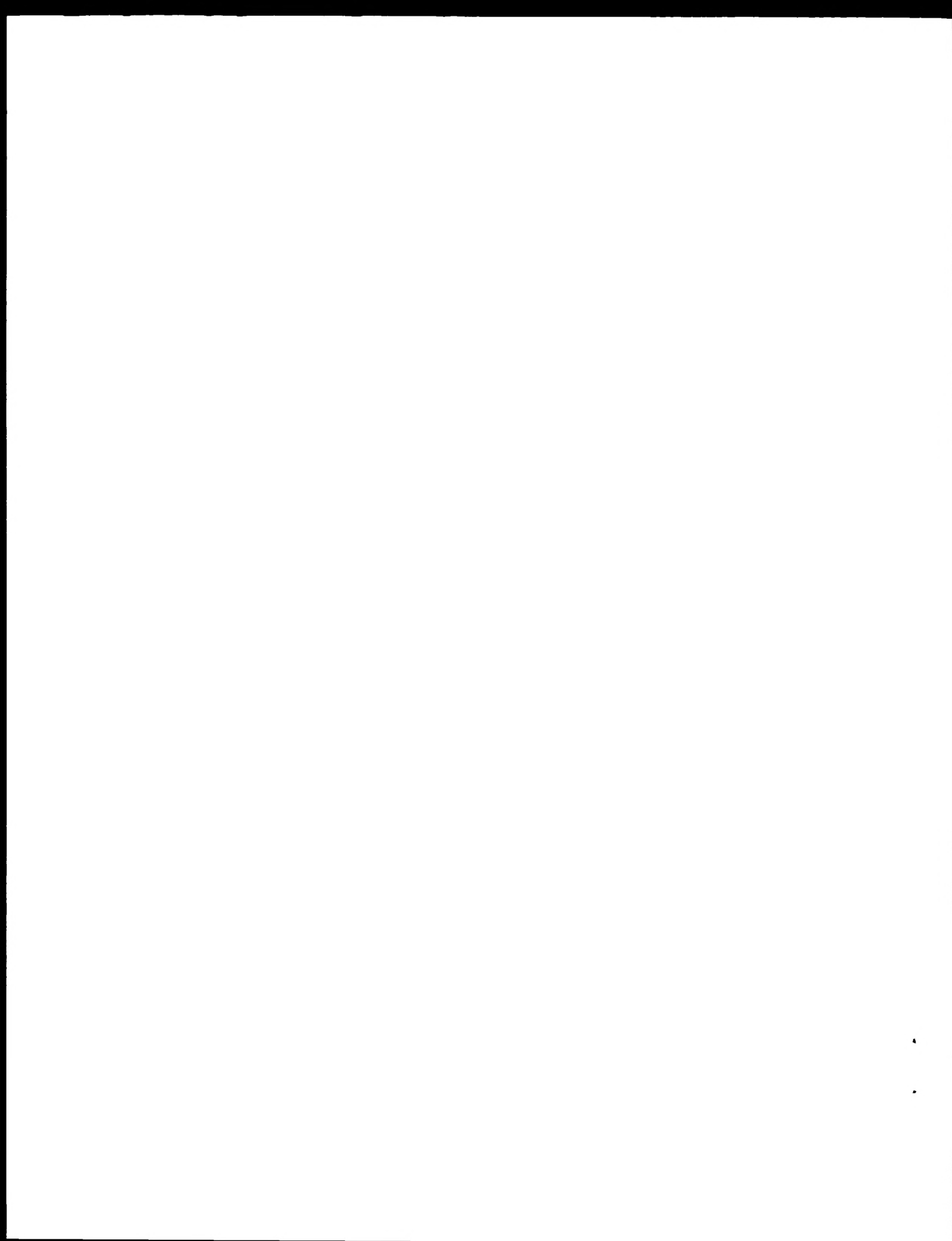
XX 08-SEP-2000.

XX		28-FEB-2000; 2000MO-US04970.	
XX			
XX	PP	Q1-NAP-1999; qnrs-0122q74	
XX	PP	05-NOV-1999; qnrs-0163q82	
XX	PP	04-MAY-1999; 99US-0457646.	
XX		(CELL-) CELL GENESYS INC.	
XX	FA	(MITO-) MITOTIX INC.	
XX			
XX	PI	Patel S, McArthur J, Gyuris J;	
XX			
XX	DR	WPI: 4300-5655sl/52.	
XX	DK	N-PStB; AAA50319.	
XX			
PPT	PT	Inhibiting angiogenesis and treating angiogenesis-associated	
PPT	PT	conditions, e.g neoplasia, psoriasis by transducing an endothelial	
PPT	PT	cell with a recombinant virus having a transgene encoding a cyclin	
PPT	PT	dependent kinase inhibitor .	
PS		Example 1: Page 127-128, 138ff, English.	
XX			
CC	CC	The present sequence is that of human p27, a cyclin dependent	
CC	CC	kinase inhibitor (Cdk1) that inhibits angiogenesis. A claimed	
CC	CC	method for inhibiting angiogenesis involves transducing an	
CC	CC	epithelial cell with a transgene encoding (internalizable,	
CC	CC	secretable) Cdk1. The delivery system for the transgene may be a	
CC	CC	liposome or a recombinant virus. The CDK1 is preferably a protein	
CC	CC	of the CIP/KIP family such as p27, a protein of the INK4 family	
CC	CC	such as p16, active fragments of these proteins (e.g. amino acids	
CC	CC	25-35 or 12-178 of human p27), or a fusion of 2 CDK1 proteins such	
CC	CC	as p27 and p16 (see AAY96068-80). The method is useful in treating	
CC	CC	conditions associated with angiogenesis, e.g. neoplasia, rheumatoid	
CC	CC	arthritis, endometriosis, psoriasis and vascular retinopathy	
CC	CC	(claimed). Alternatively, the transgene is delivered to an	
CC	CC	auxiliary cell, and is expressed by that cell such that the CDK1 is	
CC	CC	released into the blood and contacts the target epithelial cell.	
XX			
XX	SQ	Sequence 198 AA:	
		Query Match 91.4%; Score 870; DB 21; Length 198;	
		Best Local Similarity 91.0%; Pred. No. 3.6e-86;	
		Matches 162; Conservative 7; Mismatches 9; Indels 0; Gaps 0;	
QY	1	MSNVSVNGSPSLEFPADPQAQVPKPACPNIFGPNHBEELTRDLEKHRRDMEASQRKW	60
DB	1	MSNVRVNSASP-SLERMCAFLAEHPKEFSA-RNLFGPVDFHEELTKULEKHGRDMEASQRKW	60
QY	61	NP-LPHNHKLPEKKYQWEVEKSLPLFFYPFPPFKGACKVVAQESQDVSGIJKQAVPLMC	120
DB	61	NFDFOFNHKPLEGGYQWEVEKSLPLFFYPFPPPKGACKVPAQESODVSGSRPAALIG	120
QY	121	SVANSDELHLVDKIDLTADNAJSLAQCTGIKKKPAFDUSSPUNKANKIEENVSDGS	178
DB	121	AFANSEDLHLVDKIDLPSPDSUQLAKACAGIKKKKPAFDUSSFNKKANKIEENVSDGS	178
RESULT 13			
AAY44400			
ID	AA	AAY44400 standard; Protein; 198 AA.	
AC	AA	AAY44400;	
XX			
XX	DT	22-MAR-2000 (first entry)	
XX			
XX		Human p27(Kip1) kinase inhibitor protein.	
XX	KW	p27(Kip1) kinase inhibitor protein; FKBP-12; p27(Kip1). FKBP-12 complex;	
KW	KW	cytosolic drug-binding protein; Yeast two hybrid assay system;	
KW	KW	cell differentiation, apoptosis, neurodegeneration; tumorigenicity,	
KW	KW	cell proliferation related disorder; attherosclerosis, autoimmune disease;	
KW	KW	transplant rejection, inflammation, allergy, cancer, viral infection,	
KW	KW	membranous nephropathy; CDK; cyclin-dependent kinase.	

OS Homo sapiens.
XX
PN W0200075184-A1.
XX
PD 14-DEC-2000.
XX
PF 05-JUN-2000; 2000W0-US15449.
XX
PR 04-JUN-1999; 990S-0137494.
XX
PA (UYVA) UNIV YALE.
XX
PI Zhang H, Tsvetkov LM, Kondo T;
XX
DR WPI; 2001-061703/07.
DR N-PSDB; AAC84621.
XX
PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,
PT involves altering levels of proteins such as S-phase kinase associated
PT proteins 1, 2 and cullin/Cb53 proteins -
XX
PS Claim 25; Page 149-150; 162pp; English.
XX
CC The invention relates to methods of altering the polypeptide levels in a
CC cell, using proteins selected from S-phase kinase associated proteins 1
CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
CC cullin/cbc53 family of proteins). The method is useful for altering the
CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Rad of Bel-2
CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents
CC that modulate interactions between SKP and target proteins are useful for
CC treating tumours.
XX
SQ Sequence 198 AA;

Query Match 91.4%; Score 870; DB 22; Length 198;
Best Local Similarity 91.0%; Pred. NO. 3.6e-86;
Matches 162; Conservative 7; Mismatches 9; Indels 0, Gaps 0,
QY 1 MSNVVSNCSSELEPMAPAPYKPKPSACPNLEGGVNHHELTRELEKHPHMEASOKKW 50
DB 1 MSNVVSNCSSELEPMAPAPYKPKPSACPNLEGGVNHHELTRELEKHPHMEASOKKW 50
QY 61 NFEFQNHKYLEKKEVQWQVFKGSIFFYYPPPPPPKPAFYVVPAGESTQVSGTPOAVPLMG 120
DB 61 NFEFQNHKYLEKKEVQWQVFKGSIFFYYPPPPPPKPAFYVVPAGESTQVSGTPOAVPLMG 120
QY 121 SCANSEDTLVDQKTDADNAGLAECVIGIIPKPPATIGVSSPKPKRNPTEENVSDGS 178
DB 121 AFANSEDTLVDQKTDADNAGLAECVIGIIPKPPATIGVSSPKPKRNPTEENVSDGS 178

Search completed: May 30, 2003, 08:58:26
Job time : 39.0956 secs




```
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,002
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-079 03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-794-002-22

Query Match 100.0%; Score 952; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.4e-95;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSNVVNSGSPSLERMDARQAEYKPSACRNLFPGVNHHELTLDLEKRRDMEASQKWK 60
Db 1 MSNVVNSGSPSLERMDARQAEYKPSACRNLFPGVNHHELTLDLEKRRDMEASQKWK 60
QY 61 NFDQNHKPLEGKYEWQVEKGLPEFYPPPPKPKGACKVPAQESQDVSGTRQAVPLMG 120
Db 61 NFDQNHKPLEGKYEWQVEKGLPEFYPPPPKPKGACKVPAQESQDVSGTRQAVPLMG 120
QY 121 SQANSEDLHLVDQKTDADNAGLAEOCTGIRKRPATDSSPONKRANRTEENVSDGS 178
Db 121 SQANSEDLHLVDQKTDADNAGLAEOCTGIRKRPATDSSPONKRANRTEENVSDGS 178

RESULT 5
US-08-406-248-4
; Sequence 4, Application US/08/065248
; Patent No. 5736318
; GENERAL INFORMATION:
; APPLICANT: Munger, Karl
; APPLICANT: Jones, D. Leanne
; TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING
; TITLE OF INVENTION: TRANSFORMED CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ann-Louise Kerner, Ph.D., Lappin & Kusner
; STREET: 200 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,248
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: HAZ-011
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-330-1300
; TELEFAX: 617-330-1311
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-406-248-4

Query Match 91.4%; Score 870; DB 1; Length 198;
Best Local Similarity 91.0%; Pred. No. 1.1e-86;
Matches 162; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MSNVVNSGSPSLERMDARQAEYKPSACRNLFPGVNHHELTLDLEKRRDMEASQKWK 60
Db 1 MSNVVNSGSPSLERMDARQAEYKPSACRNLFPGVNHHELTLDLEKRRDMEASQKWK 60
QY 61 NFDQNHKPLEGKYEWQVEKGLPEFYPPPPKPKGACKVPAQESQDVSGTRQAVPLMG 120
Db 61 NFDQNHKPLEGKYEWQVEKGLPEFYPPPPKPKGACKVPAQESQDVSGTRQAVPLMG 120
QY 121 SQANSEDLHLVDQKTDADNAGLAEOCTGIRKRPATDSSPONKRANRTEENVSDGS 178
Db 121 SQANSEDLHLVDQKTDADNAGLAEOCTGIRKRPATDSSPONKRANRTEENVSDGS 178

RESULT 6
US-08-897-333A-2
; Sequence 2, Application US/08897333A
; Patent No. 6177272
; GENERAL INFORMATION:
; APPLICANT: Nabel, Gary J
; APPLICANT: Nabel, Elizabeth G.
; TITLE OF INVENTION: METHOD FOR INHIBITING VASCULAR PROLIFERATIVE DISEASES
; TITLE OF INVENTION: WITH p27 AND FUSIONS THEREOF
; FILE REFERENCE: 8642/4
; CURRENT APPLICATION NUMBER: US/08/897,333A
; CURRENT FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-897-333A-2
```

```
Query Match 91.4%; Score 870; DB 4; Length 198;
Best Local Similarity 91.0%; Pred. No. 1.1e-86;
Matches 162; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MSNVVNSGSPSLERMDARQAEYKPSACRNLFPGVNHHELTLDLEKRRDMEASQKWK 60
Db 1 MSNVVNSGSPSLERMDARQAEYKPSACRNLFPGVNHHELTLDLEKRRDMEASQKWK 60
QY 61 NFDQNHKPLEGKYEWQVEKGLPEFYPPPPKPKGACKVPAQESQDVSGTRQAVPLMG 120
Db 61 NFDQNHKPLEGKYEWQVEKGLPEFYPPPPKPKGACKVPAQESQDVSGTRQAVPLMG 120
QY 121 SQANSEDLHLVDQKTDADNAGLAEOCTGIRKRPATDSSPONKRANRTEENVSDGS 178
Db 121 SQANSEDLHLVDQKTDADNAGLAEOCTGIRKRPATDSSPONKRANRTEENVSDGS 178

RESULT 7
US-09-240-906-6
; Sequence 6, Application US/09240906
; Patent No. 6245965
; GENERAL INFORMATION:
; APPLICANT: ROUSSEL, MARTINE F.
; APPLICANT: SNEYNE, RICHARD
; APPLICANT: ZINDY, FREDERIQUE
```


EARLIER APPLICATION NUMBER: 60/122,974
EARLIER FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 26
LENGTH: 198
TYPE: PRT
ORGANISM: Homo sapiens
US-09-457-646-26

Query Match 91.4%; Score 870; DB 4; Length 198;
Best Local Similarity 91.0%; Pred. No. 1.1e-86;
Matches 162; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MSNVRVNSGSPSLERMDARQAEYKPKPSACPNLFPGVNHHEELTPDLEKHRRDMEASQKKN 60
DB 1 MSNVRVNSGSPSLERMDARQAEYKPKPSACPNLFPGVNHHEELTPDLEKHRRDMEASQKKN 60
QY 61 NEFQNHKPLEKYEWEVEKSLPEFYYPKPKPKGA:KVPAPLSLVSOTROAVPLMG 120
DB 61 NEFQNHKPLEKYEWEVEKSLPEFYYPKPKPKGA:KVPAPLSLVSOTROAVPLMG 120
QY 121 SOANSEDTLHVQKTDIALNQAAGLAECQCTGIPKRPATDDSSPKNRANPTEENVSDGS 178
DB 121 SOANSEDTLHVQKTDIALNQAAGLAECQCTGIPKRPATDDSSPKNRANPTEENVSDGS 178

RESULT 11
US-08-589-981-2
Sequence 2, Application US/08589981
Patent No. 5672508
GENERAL INFORMATION:
APPLICANT: Gyuris, Jeno
APPLICANT: Lamphere, Lou
APPLICANT: Beach, David H.
TITLE OF INVENTION: Inhibitors of Cell-Cycle Progression,
TITLE OF INVENTION: and Uses Related Thereto
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & JACKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,981
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: M11-069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-589-981-2

Query Match 90.9%; Score 865; DB 1; Length 391;
Best Local Similarity 91.0%; Pred. No. 9.7e-86;
Matches 161; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 2 SNRVNSGSPSLERMDARQAEYKPKPSACPNLFPGVNHHEELTPDLEKHRRDMEASQKKN 61
DB 8 SNRVNSGSPSLERMDARQAEYKPKPSACPNLFPGVNHHEELTPDLEKHRRDMEASQKKN 67
QY 62 FDFQNHKPLEKYEWEVEKSLPEFYYPKPKPKGA:KVPAPLSLVSOTROAVPLMG 121
DB 62 FDFQNHKPLEKYEWEVEKSLPEFYYPKPKPKGA:KVPAPLSLVSOTROAVPLMG 127
QY 122 QANSEDTLHVQKTDIALNQAAGLAECQCTGIPKRPATDDSSPKNRANPTEENVSDGS 178
DB 122 QANSEDTLHVQKTDIALNQAAGLAECQCTGIPKRPATDDSSPKNRANPTEENVSDGS 184

RESULT 12

US-09-457-568-4
Sequence 4, Application US/09457568
Patent No. 6413943
GENERAL INFORMATION:
APPLICANT: McArthur, James G
APPLICANT: Gyuris, Jeno
APPLICANT: Finer, Mitchell H.
TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
TITLE OF INVENTION: Smooth Muscle Cells
FILE REFERENCE: 106482.691
CURRENT APPLICATION NUMBER: US/09/457,568
EARLIER FILING DATE: 1999-12-09
EARLIER APPLICATION NUMBER: 60/122,974
EARLIER FILING DATE: 1999-03-01
EARLIER APPLICATION NUMBER: 60/163,682
EARLIER FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 391
TYPE: PRT
ORGANISM: Homo sapiens
US-09-457-568-4

Query Match 90.9%; Score 865; DB 4; Length 391;
Best Local Similarity 91.0%; Pred. No. 9.7e-86;
Matches 161; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 2 SNRVNSGSPSLERMDARQAEYKPKPSACPNLFPGVNHHEELTPDLEKHRRDMEASQKKN 61
DB 8 SNRVNSGSPSLERMDARQAEYKPKPSACPNLFPGVNHHEELTPDLEKHRRDMEASQKKN 67
QY 62 FDFQNHKPLEKYEWEVEKSLPEFYYPKPKPKGA:KVPAPLSLVSOTROAVPLMG 121
DB 62 FDFQNHKPLEKYEWEVEKSLPEFYYPKPKPKGA:KVPAPLSLVSOTROAVPLMG 127
QY 122 QANSEDTLHVQKTDIALNQAAGLAECQCTGIPKRPATDDSSPKNRANPTEENVSDGS 178
DB 122 QANSEDTLHVQKTDIALNQAAGLAECQCTGIPKRPATDDSSPKNRANPTEENVSDGS 184

RESULT 13

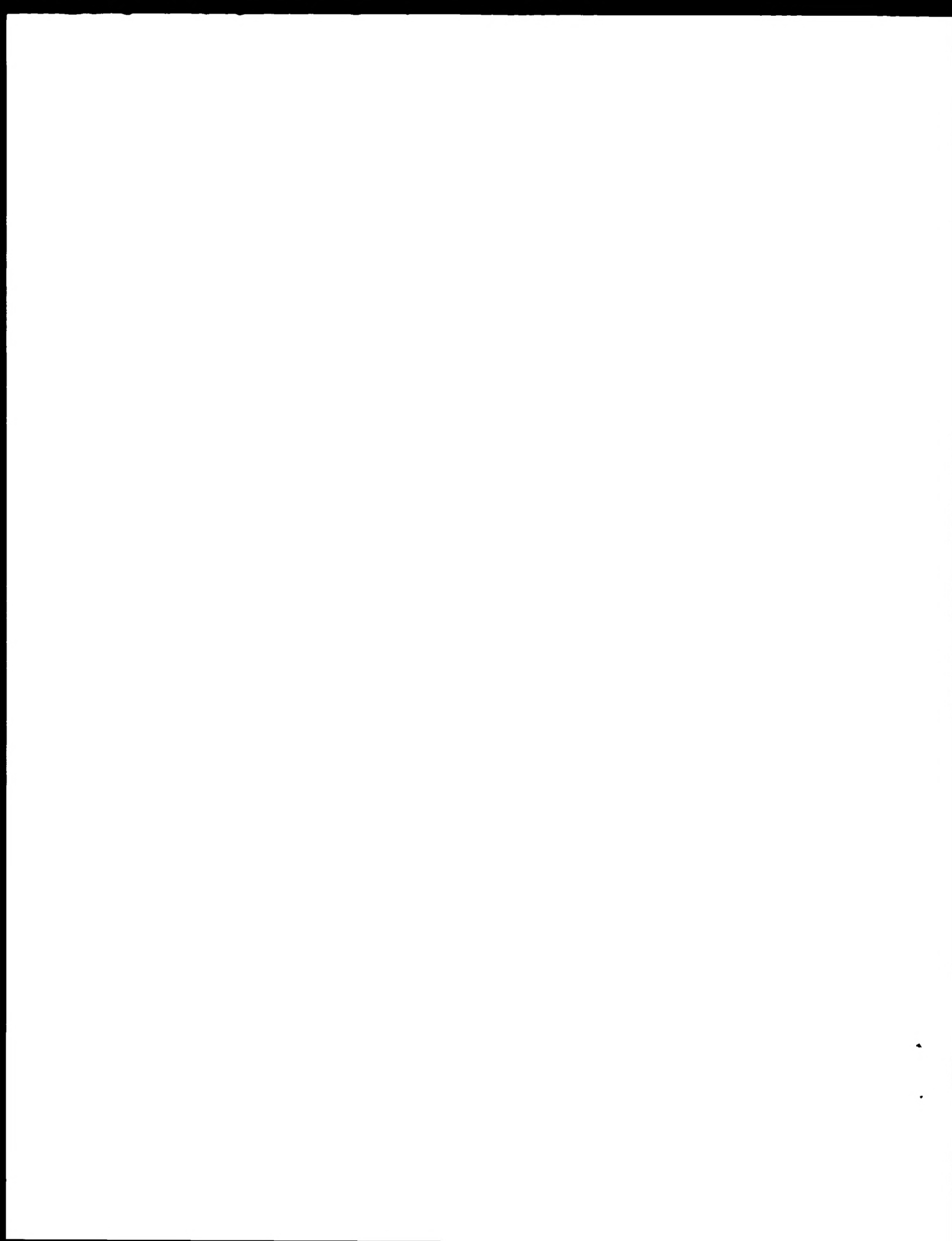
US-09-457-646-4
Sequence 4, Application US/09457646
Patent No. 6420345
GENERAL INFORMATION:
APPLICANT: Patel, Salil D
APPLICANT: McArthur, James G
APPLICANT: Gyuris, Jeno
TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
TITLE OF INVENTION: Smooth Muscle Cells
FILE REFERENCE: 106482.287
CURRENT APPLICATION NUMBER: US/09/457,646
CURRENT FILING DATE: 1999-12-09
EARLIER APPLICATION NUMBER: 60/122,974
EARLIER FILING DATE: 1999-03-01
EARLIER APPLICATION NUMBER: 60/163,682
EARLIER FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 32

Mon Jun 2 17:01:11 2003

us-09-865-018b-6.ra1

Page 7

Search completed: May 30, 2003, 09:03:44
Job time : 13.3385 secs



GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd

OM protein - protein search, using sw model

Run on: May 30, 2003, 08:58:52 : Search time 18.18 seconds
(without alignments)
991 716 Million cell updates/sec

Title: US-09-865-018b-6

Perfect score: 952

Sequence: 1 MSNVRVSGNSPSTPMHAPQ DSSPNKPANPTENVSDGS 178

Scoring table: BIOSW62

Gapop 10.0 : Gapext 0.5

Search-J: 383519 seqs, 10122664 residues

Total number of hits satisfying chosen parameters: 322519

Minimum DB seq length: 6

Maximum DB seq length: 200000000

Post-processing: Minimum Match 8%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cqn2-6/ptodata/1/pubpaa/US08_NEW_PUB pep:*
2: /cqn2-6/ptodata/1/pubpaa/PCT_NEW_PUB pep:*
3: /cqn2-6/ptodata/1/pubpaa/US06_NEW_PUB pep:*
4: /cqn2-6/ptodata/1/pubpaa/US06_PUBCOMB pep:*
5: /cqn2-6/ptodata/1/pubpaa/US07_NEW_PUB pep:*
6: /cqn2-6/ptodata/1/pubpaa/US07_PUBCOMB pep:*
7: /cqn2-6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep:*
8: /cqn2-6/ptodata/1/pubpaa/US08_PUBCOMB pep:*
9: /cqn2-6/ptodata/1/pubpaa/US09_NEW_PUB pep:*
10: /cqn2-6/ptodata/1/pubpaa/US09_PUBCOMB pep:*
11: /cqn2-6/ptodata/1/pubpaa/US10_NEW_PUB pep:*
12: /cqn2-6/ptodata/1/pubpaa/US10_PUBCOMB pep:*
13: /cqn2-6/ptodata/1/pubpaa/US60_NEW_PUB pep:*
14: /cqn2-6/ptodata/1/pubpaa/US60_PUBCOMB pep:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	952	100.0	178	10	US-09-865-018b-6 Sequence 6, Appl
2	872	91.4	198	9	US-09-970-661-2 Sequence 2, Appl
3	865	90.9	391	8	US-08-902-572-2 Sequence 2, Appl
4	863	90.7	194	10	US-09-865-018b-2 Sequence 8, Appl
5	860	90.3	365	8	US-08-902-572-8 Sequence 6, Appl
6	860	90.3	380	8	US-08-902-572-6 Sequence 4, Appl
7	846	88.9	197	8	US-09-865-018b-4 Sequence 18, Appl
8	811	85.2	167	8	US-08-902-572-19 Sequence 23, Appl
9	811	85.2	334	8	US-08-902-572-20 Sequence 24, Appl
10	811	85.2	348	8	US-08-902-572-24 Sequence 26, Appl
11	390.5	41.0	237	8	US-08-902-572-25 Sequence 20, Appl
12	386	40.5	252	8	US-08-902-572-28 Sequence 20, Appl
13	377	39.6	76	8	US-08-902-572-29 Sequence 770, App
14	167.5	17.6	247	13	US-09-945-297-719 Sequence 4, Appl
15	163	17.1	164	9	US-09-221-268-3 Sequence 5, Appl
16	163	17.1	164	4	US-09-221-268-5 Sequence 24, Appl
17	163	17.1	164	10	US-09-865-018b-24 Sequence 2, Appl
18	163	17.1	164	10	US-09-940-766-2 Sequence 2, Appl
19	100	10.6	191	10	US-09-733-507-2

Sequence 10, Appl
Sequence 12, Appl
Sequence 266, App
Sequence 15, Appl
Sequence 159, App
Sequence 15, Appl
Sequence 14, Appl
Sequence 470, App
Sequence 16, Appl
Sequence 36182, A
Sequence 527, App
Sequence 14, Appl
Sequence 61, Appl
Sequence 1, Appl
Sequence 62, Appl
Sequence 2, Appl
Sequence 60, Appl
Sequence 12955, A
Sequence 8, Appl
Sequence 158, App
Sequence 2, Appl
Sequence 3, Appl
Sequence 8, Appl
Sequence 212, App
Sequence 148, App

ALIGNMENTS

RESULT 1

US-09-865-018b-6
Sequence 6, Application US/09865018
Patent No. US20020110866A1
GENERAL INFORMATION:

APPLICANT: Massague, Joan
Roberts, James M.
Koff, Andrew
Polysak, Kornelia

TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHOD FOR ITS
PRODUCTION AND USE

NUMREP OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/865,018

FILING DATE: 24-May 2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/854,039

FILING DATE: 09-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: MIV-079-04

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-832-1000

TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 178 amino acids

TYPE: amino acid

TOPOLOGY: linear

;; FILING DATE: 24 MAY 2001
;; PRIOR APPLICATION DATA: US/08/854,039
;; APPLICATION NUMBER: US/08/854,039
;; FILING DATE: 09-MAY-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Vincent, Matthew P.
;; REGISTRATION NUMBER: 36,709
;; REFERENCE/DOCKET NUMBER: MIV-079.04
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-832-1000
;; TELEFAX: 617-832-7000
;; INFORMATION FOR SEQ ID NO: 2:
;; SPOTEN/F CHARACTERISTICS:
;; LENGTH: 198 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-865-018b-2

Query Match
Best Local Similarity 90.7%; Score 863; DB 10; Length 198;
Matches 161; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSNVSVNSGSPSLFMDAPQAEYKPKPSACRNLPQVNHHELTPTLEKHPDMEASQPKW 60
Db 1 MSNVSVNSGSPSLFMDAPQAEYKPKPSACRNLPQVNHHELTPTLEKHPDMEASQPKW 60

QY 61 NFDGNHKKPLECKYEQVEKGSLEPEFYRPPRPKPKGACKVPAQESQVSTKQAVPLMG 120
Db 61 NFDGNHKKPLECKYEQVEKGSLEPEFYRPPRPKPKGACKVPAQESQVSTKQAVPLMG 120

QY 121 SCANSEDLHLVDKTDITADNAGLAEOCTGIRKRPATDDSSPQNKRRANRTEENVSDGS 178
Db 121 SCANSEDLHLVDKTDITADNAGLAEOCTGIRKRPATDDSSPQNKRRANRTEENVSDGS 178

RESULT 5
US-08-902-572-8
; Sequence 8, Application US/08902572
; Patent No. US20020068706A1
; GENERAL INFORMATION:
; APPLICANT: Gyuris, Jeni
; APPLICANT: Lamphere, Lou
; APPLICANT: Beach, David H.
; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
; TITLE OF INVENTION: RELATED THERETO
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,572
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-069.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-902-572-6

Query Match
Best Local Similarity 90.4%; Score 860; DB 8; Length 365;
Matches 160; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 2 SNVPVNSGSPSLFMDAPQAEYKPKPSACRNLPQVNHHELTPTLEKHPDMEASQPKW 61
Db 2 SNVPVNSGSPSLFMDAPQAEYKPKPSACRNLPQVNHHELTPTLEKHPDMEASQPKW 61

QY 62 FDFQNHKKPLECKYEQVEKGSLEPEFYRPPRPKPKGACKVPAQESQVSTKQAVPLMG 121
Db 62 FDFQNHKKPLECKYEQVEKGSLEPEFYRPPRPKPKGACKVPAQESQVSTKQAVPLMG 121

QY 229 FDFQNHKKPLECKYEQVEKGSLEPEFYRPPRPKPKGACKVPAQESQVSTKQAVPLMG 288
Db 229 FDFQNHKKPLECKYEQVEKGSLEPEFYRPPRPKPKGACKVPAQESQVSTKQAVPLMG 288

QY 122 QANSEDLHLVDKTDITADNAGLAEOCTGIRKRPATDDSSPQNKRRANRTEENVSDGS 178
Db 122 QANSEDLHLVDKTDITADNAGLAEOCTGIRKRPATDDSSPQNKRRANRTEENVSDGS 178

;; LENGTH: 365 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-902-572-8

Query Match
Best Local Similarity 90.3%; Score 860; DB 8; Length 365;
Matches 160; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 2 SNVPVNSGSPSLFMDAPQAEYKPKPSACRNLPQVNHHELTPTLEKHPDMEASQPKW 61
Db 2 SNVPVNSGSPSLFMDAPQAEYKPKPSACRNLPQVNHHELTPTLEKHPDMEASQPKW 61

QY 62 FDFQNHKKPLECKYEQVEKGSLEPEFYRPPRPKPKGACKVPAQESQVSTKQAVPLMG 121
Db 62 FDFQNHKKPLECKYEQVEKGSLEPEFYRPPRPKPKGACKVPAQESQVSTKQAVPLMG 121

QY 229 FDFQNHKKPLECKYEQVEKGSLEPEFYRPPRPKPKGACKVPAQESQVSTKQAVPLMG 288
Db 229 FDFQNHKKPLECKYEQVEKGSLEPEFYRPPRPKPKGACKVPAQESQVSTKQAVPLMG 288

QY 122 QANSEDLHLVDKTDITADNAGLAEOCTGIRKRPATDDSSPQNKRRANRTEENVSDGS 178
Db 122 QANSEDLHLVDKTDITADNAGLAEOCTGIRKRPATDDSSPQNKRRANRTEENVSDGS 178

RESULT 6
US-08-902-572-6
; Sequence 6, Application US/08902572
; Patent No. US20020068706A1
; GENERAL INFORMATION:
; APPLICANT: Gyuris, Jeni
; APPLICANT: Lamphere, Lou
; APPLICANT: Beach, David H.
; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
; TITLE OF INVENTION: RELATED THERETO
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,572
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-069.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-902-572-6

Query Match
Best Local Similarity 90.4%; Score 860; DB 8; Length 390;
Matches 160; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 2 SNVPVNSGSPSLFMDAPQAEYKPKPSACRNLPQVNHHELTPTLEKHPDMEASQPKW 61
Db 2 SNVPVNSGSPSLFMDAPQAEYKPKPSACRNLPQVNHHELTPTLEKHPDMEASQPKW 61

QY 184 SNVPVNSGSPSLFMDAPQAEYKPKPSACRNLPQVNHHELTPTLEKHPDMEASQPKW 243
Db 184 SNVPVNSGSPSLFMDAPQAEYKPKPSACRNLPQVNHHELTPTLEKHPDMEASQPKW 243


```

; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/902,572
; APPLICATION NUMBER: US/08/902,572
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-069,03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 22
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-902-572-22

Query Match 85.2%; Score 811; DB 8; Length 334;
Best Local Similarity 90.4%; Pred. No. 5, 1e-69;
Matches 150; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 12 SLEPMACACAEYFKISACPNLFGPVNHEELTDLKHKRPDMEEASQKWNFDQNHKPLE 71
DB 12 SLEPMACACAEYFKISACPNLFGPVNHEELTDLKHKRPDMEEASQKWNFDQNHKPLE 71
QY 72 GKYEWQVEKSLPEFYYPKPPKGAQKVAQESQVSGTRQAVPLMSQANSEDTHLV 141
DB 72 GKYEWQVEKSLPEFYYPKPPKGAQKVAQESQVSGTRQAVPLMSQANSEDTHLV 131
QY 132 DQKIDTADNAGIAEQCTGIRKRPATDSSPQNKPRANRTEENVSDG 177
DB 132 DPKTDPDSQTLAEQCAQIRKRPATDSSPQNKPRANRTEENVSDG 177

RESULT 10
US-08-902-572-24
; Sequence 24, Application US/08/902,572
; Patent No. US2002008706A1
; GENERAL INFORMATION:
; APPLICANT: Gyuris, Jeno
; APPLICANT: Lamphere, Lou
; APPLICANT: Beach, David H.
; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
; TITLE OF INVENTION: RELATED THERETO
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,572
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-069,03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 26;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-902-572-24

Query Match 85.2%; Score 811; DB 8; Length 334;
Best Local Similarity 90.4%; Pred. No. 5, 1e-69;
Matches 150; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 12 SLEPMACACAEYFKISACPNLFGPVNHEELTDLKHKRPDMEEASQKWNFDQNHKPLE 71
DB 12 SLEPMACACAEYFKISACPNLFGPVNHEELTDLKHKRPDMEEASQKWNFDQNHKPLE 71
QY 72 GKYEWQVEKSLPEFYYPKPPKGAQKVAQESQVSGTRQAVPLMSQANSEDTHLV 141
DB 72 GKYEWQVEKSLPEFYYPKPPKGAQKVAQESQVSGTRQAVPLMSQANSEDTHLV 131
QY 132 DQKIDTADNAGIAEQCTGIRKRPATDSSPQNKPRANRTEENVSDG 177
DB 132 DPKTDPDSQTLAEQCAQIRKRPATDSSPQNKPRANRTEENVSDG 177

RESULT 11
US-08-902-572-26
; Sequence 26, Application US/08/902,572
; Patent No. US2002008706A1
; GENERAL INFORMATION:
; APPLICANT: Gyuris, Jeno
; APPLICANT: Lamphere, Lou
; APPLICANT: Beach, David H.
; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
; TITLE OF INVENTION: RELATED THERETO
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,572
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-069,03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 26;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-902-572-24
```


TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (131)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-247-770

Query Match 17 68; Score 167 5; DR 10; Length 247;
Best Local Similarity 27.9%; Pred No 3 4e-08;
Matches 48; Conservative 24; Mismatches 75; Indels 25; Gaps 4;
QY 3 NVRVSGSPSIFPMIAPQAEYFKESACHNLEGGVNHHELTROLEKHHEDMEASORKNWF 62
DB 84 HVRTGWGCTSE-----EMPHKACDFEFGPVSEQLSDCLMAGCIGQEAEXWNF 134
QY 63 PFQNHKPLEGKYFWQVEKSGSLPEFYPPPPPKGACKVPAQESQDVSGTRQAVPLMGSK 122
DB 135 DAVTRPLEGDFAWKVRGICGPKLYL-PVGPFRGRDELG-----GGPPPGTSPALLQ 186
QY 123 ANSELT-----LVQKTTTADNAGLAEGTETGKHKVAUHUSSPQKP 165
DB 187 GTAEETHVLSITTLVPSKEDAFSSPGPRLSGKPKPKLSMTDFYHSKP 238

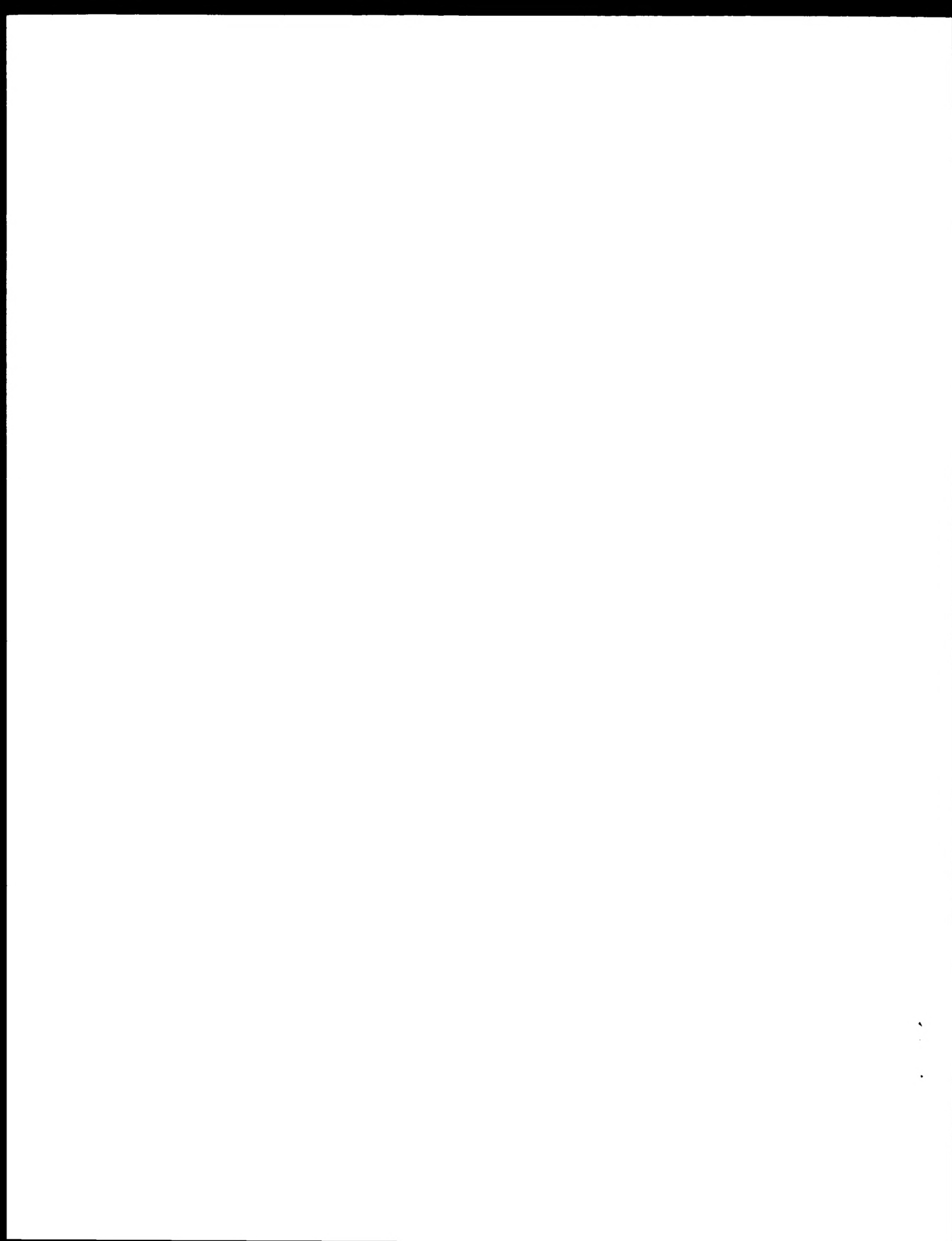
RESULT 15

US-09-221-268-3
Sequence 3; Application US/09221268A
Publication No. US20020183509A1
GENERAL INFORMATION:
APPLICANT: Fisher, Paul B. and
APPLICANT: Jiang, Hongping
APPLICANT: The Trustees of Columbia University in the City of New York
TITLE OF INVENTION: METHOD FOR GENERATING A SUBTRACTED cDNA LIBRARY AND
TITLE OF INVENTION: USES OF THE GENERATED LIBRARY
FILE REFERENCE: 0575/43563-B
CURRENT APPLICATION NUMBER: US/09/221-268A
CURRENT FILING DATE: 1998-12-23
EARLIER APPLICATION NUMBER: 08/316,537
EARLIER FILING DATE: 1994-09-10
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 3
LENGTH: 164
TYPE: PRT
ORGANISM: MDA-6(2)
US-09-221-268-3

Query Match 17 18; Score 163; DR 9; Length 164;
Best Local Similarity 28 68; Pred No 5 3e-08;
Matches 42; Conservative 23; Mismatches 66; Indels 16; Gaps 3;
QY 28 ACNRLPGPVNHELTROLEKHHEDMEASORKNWFDFONHKPLEGKYBQVEKSGSLPEF 87
DB 17 ACNRLPGPVDSQISWDCLMAGCIGQEAERWNEFVTETPLEDFAWKVRGLGLPKL 76
QY 88 YVEPPPPKGA'KVPAQESQDVSGTRQAVPLMGSKANSEDT-----LVQKTTDAD 139
DB 77 YL-PTGPRGRDELG-----GGPPPGTSPALLQGTAEETHVLSITTLVPSKEDAFSSPGPRLSGKPKPKLSMTDFYHSKP 128
QY 140 NUAGLAFQCTGIRKRPATDSSPQKP 166
DB 129 GSPGPGTSGQPKPKPKLSMTDFYHSKP 155

Search completed: May 30, 2004, 09:05:12
Job time : 19.168 secs

[illegible][illegible][illegible][illegible][illegible][illegible]



GenCore version 5.1.6
Copyright (c) 1993 - 2003 CarpuGen Ltd

OM protein - protein search, using sw model

Run on: May 30, 2003, 08:52:42 : Search time 7 s 9015 seconds
(without alignments)
972.608 Million cell updates/sec

Title: US-09-865-018B-6
Perfect score: 952
Sequence: 1 MSNVRVNSGSPSTERMDARQ.....DSSPQNKRNKRNENVDGS 178

Scoring table: BLOSUM62
Gapop 10 0 , Gapext 0.5

Searched: 112892 seqs, 41475328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	952	100	0	1 CNRB_MUSVI	P45529 mustela vis
2	919	96.5	198	1 CNRB_FELCA	O19001 felis silve
3	870	91.4	198	1 CNRB_HUMAN	P45527 homo sapien
4	855	89.8	197	1 CNRB_MOUSE	P46414 mus musculu
5	838	88.0	198	1 CNRB_CRIGR	Q60439 cricetulus
6	196.5	20.6	316	1 CNRB_HUMAN	P49918 homo sapien
7	191	20.1	348	1 CNRB_MOUSE	P49919 mus musculu
8	168.5	17.7	159	1 CNRB_MOUSE	P39689 mus musculu
9	166.5	17.5	164	1 CNRB_FELCA	Q52002 felis silve
10	163	17.1	164	1 CNRB_HUMAN	P38936 homo sapien
11	89.5	9.4	514	1 WRK3_ARATH	Q61600 arabidopsis
12	89	9.3	548	1 KRCR_MOUSE	P70194 mus musculu
13	86	9.0	914	1 PBPA_BACSU	P39793 bacillus su
14	85.5	9.0	937	1 N198_PAT	P49793 rattus norv
15	84.5	8.9	236	1 Y126_YEAST	P47115 saccharomyc
16	84.5	8.9	369	1 MX_STRPY	P16946 streptococ
17	84.5	8.9	894	1 RPN2_YEAST	P42786 saccharomyc
18	84.5	8.9	1231	1 YRT3_CAEEL	P43114 caenorhabdi
19	84	8.8	801	1 BRD2_HUMAN	P25440 homo sapien
20	84	8.8	1969	1 MYSA_CAFEL	P27844 caenorhabdi
21	84	8.8	2033	1 PVF1_HUMAN	Q62817 homo sapien
22	83.5	8.8	735	1 ALGA_KAI	Q63028 rattus norv
23	83.5	8.8	1014	1 HX2_YEAST	Q00816 saccharomyc
24	83	8.7	2472	1 ATRX_HUMAN	P46100 homo sapien
25	82.5	8.7	857	1 NFM_CHICK	P16053 gallus gall
26	82	8.6	258	1 TRT3_PAT	P09739 rattus norv
27	82	8.6	494	1 RPS5_YEAS1	P33235 saccharomyc
28	81	8.5	697	1 YP9C_SCHIN	O13773 schizosach
29	80	8.4	1109	1 TCF8_PAT	Q62947 rattus norv
30	79.5	8.4	1020	1 RPN_HUMAN	P12036 homo sapien
31	79.5	8.4	1839	1 CYAA_SACKL	P23466 saccharomyc
32	79	8.3	450	1 INVO_LEMCA	P14590 lemur catta
33	79	8.3	475	1 CAF1_HUMAN	Q61518 homo sapien

ALIGNMENTS

RESULT 1	CDNB_MUSVI	STANDARD;	PRT;	178 AA.
34	79	8 3	631	1 XPC1_MOUSE
35	79	8 3	2441	1 CRP_MOUSE
36	78.5	8 2	937	1 N198_HUMAN
37	78.5	8 2	1167	1 Z02_MOUSE
38	78.5	8 2	1210	1 AF4_HUMAN
39	78.5	8 2	1493	1 M3K1_MOUSE
40	78.5	8 2	3149	1 TEGU_EBV
41	78	8 2	261	1 XC92_HAEIN
42	78	8 2	513	1 WRK3_ARATH
43	78	8 2	536	1 ZF44_PAT
44	78	8 2	559	1 ENL_HUMAN
45	77.5	8 1	561	1 TARA_MOUSE

060596 mus musculu
 P45481 mus musculu
 P52948 homo sapien
 Q92011 mus musculu
 P51825 homo sapien
 P53349 mus musculu
 P03186 epstein-bar
 P44154 haemophilus
 Q92970 arabidopsis
 Q92XK3 rattus norv
 Q03111 homo sapien
 Q99KW3 mus musculu

CDNB_MUSVI
 A1 146534
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase inhibitor p27) (p27Kip1) (Fragment).
 GN CKN1B.
 OS Mustela vison (American mink).
 CC Eukaryota, Metazoa, Chordata, Claviata, Vertebrata, Euteleostomi;
 CC Mammalia, Eutheria, Carnivora, Fissipedia; Mustelidae; Mustelinae;
 CC Mustela.
 CC NCBI_LaXID=96b7;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=94306518; PubMed=9033212;
 RA Polyak K., Lee M.-H., Erdjument-Bromage H., Koff A., Roberts J.M., Tempst P., Massague J.;
 RT "Cloning of p27Kip1, a cyclin-dependent kinase inhibitor and a potential mediator of extracellular antimitogenic signals.";
 RL Cell 78:59-66(1994).
 RN [2]
 PP MEDLINE=94116862; PubMed=8288131;
 RA Polyak K., Kato J.-Y., Solomon M.J., Sherr C.J., Massague J., Roberts J.M., Koff A.;
 RT "p27Kip1, a cyclin-cdk inhibitor, links transforming growth factor-beta and c-myc inhibition to cell cycle arrest";
 RL Genes Dev. 8:922(1994).
 CC -1- FUNCTION: Involved in G1 arrest. May mediate TGF beta-induced G1 arrest. Binds to and inhibits complexes formed by cyclin E-CDK2, cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin NUP50 is required for nuclear import and for degradation of phosphorylated p27Kip1 after nuclear import (By similarity).
 CC -1- SUBUNIT: Interacts with NUP50 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: THE N-TERMINAL OF CIP1 AND FIP APE SIMILAR.
 CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).
 CC LMBL: Q99466, AAA00234.1.
 DE InterPro: IPR003175; CDI.
 DE Pfam: PF02234; CDI; 1.
 KW Cell cycle, Nuclear protein.
 FT DOMAIN 153 169 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
 FT NON_TER 178 178
 PP SEQUENCE 178 AA: 20129 MW: 20104 kDa: 473k cPC64;

RT with human cancer."
 RL Hum. Mol. Genet. 4:1089-1092(1995).
 RN [18]
 RP SEQUENCE FROM N.A., AND VARIANT ARG-41.
 RA Rieder M.J., Brann A.C., Montoya M.A., Chung M.-W., Nguyen C.P.,
 RA Nguyen P.A., Livingston R.J., Pei C.L., Robertson P.D.,
 RA Schackwitz W.S., Shewach M.R., Wilk L.A., Nickerson J.A.,
 RL Submitted (APR-2002) to the ENRI/GenBank/DBJ databases.
 RN [19]
 RP SEQUENCE FROM N.A.
 RA Palmer S.J.
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP SEQUENCE FROM N.A., AND VARIANT ARG-41.
 RC TISSUE: Eye, and Lung;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 149-166
 PX MFDLNF-G7015045; PubMed=8461913;
 RA Gullis J.M., Kelman Z., Hattwig T., O'Connell M., Kuriyan J.;
 RL "Structure of the C-terminal region of p21(WAF1/CIP1) complexed with
 RT human pRb".
 RT Cell 97:247-256(1998)
 CC -1- FUNCTION: MAY BE THE IMPORTANT INTERMEDIATE BY WHICH P53 MEDIATES
 CC ITS ROLE AS AN INHIBITOR OF CELLULAR PROLIFERATION IN RESPONSE TO
 CC DNA DAMAGE. MAY BIND TO AND INHIBIT CYCLIN-DEPENDENT KINASE
 CC ACTIVITY, PREVENTING PHOSPHORYLATION OF CRITICAL CYCLIN-DEPENDENT
 CC KINASE SUBSTRATES AND BLOCKING CELL CYCLE PROGRESSION.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: IS EXPRESSED IN ALL ADULT HUMAN TISSUES.
 CC WITH 5-FOLD LOWER LEVELS OBSERVED IN THE BRAIN.
 CC -1- INDUCTION: BY P53, MEZEREIN (ANTI-LEUKEMIC COMPOUND) AND INTERFERON
 CC BETA.
 CC -1- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR
 CC -1- DATABASE: NAME=Atlas Genet. Cytopher. Oncol. Haematol.;
 CC WWW="http://www.intebiochem.fr/services/chromancer/genes/ATLAS149.html"
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by individual institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See [http://www.isb-sib.ch/announcements/](http://www.isb-sib.ch/announcements)
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J25610; AAA16109.1;
 DR EMBL: X67488; AAR29246.1;
 DR EMBL: U09579; AAR55641.1;
 DR EMBL: U04106; AAC04313.1;
 DR EMBL: J26145; AAA19811.1;
 DR EMBL: J47233; AAB59560.1; ALT_INIT.
 DR EMBL: AF497972; AAM11787.1;
 DR EMBL: Z65996; CAB06856.1;
 DR EMBL: BC000275; AAH00275.1;
 DR EMBL: BC000312; AAH00412.1;
 DR EMBL: BC001935; AAH01935.1;
 DR EMBL: BC014957; AAH13957.1;
 DR PIR: S39357; S39357.
 DR SWISS-2PAGE: P38936; HUMAN.
 DR Genew: HGNC:1784; CDRN1A.
 DR MIM: 116899;
 DR InterPro: IPR003175; CDI
 DR Pfam: PF02214; CDI; 1.
 KW Cell cycle; Nuclear protein; Zinc finger; Polymorphism
 FT ZN_FING 13 41
 FT DOMAIN 141 156
 FT VARIANT 31 31
 FT SEQUENCE 164 AA; 16119 MW; 980167651467644 CRC64;
 SQ
 Query Match 17.1%; Score 163; DB 1; Length 164;
 Best Local Similarity 28.6%; E-Val. No. 5.4e-07;

Matches 42, Conservative 23, Mismatches 66; Indels 16; Gaps 3;
 QY 28 ACRNLCFVNHEELTRDLKHKRDMEEASOKKWNHFNQNHKPLEGKYENQVEKGSLEPF 87
 DB ||| ||||| ||||| : : : ||||| ||||| : : : |||
 QY 17 ACPKKEGPNVSEGLSPQIALMAGGTCFAPRNWDFVTFTPLFGDFAWERVGLGPKL 76
 DB ||| ||||| ||||| : : : ||||| ||||| : : : |||
 QY 88 YPPPPPPPKGAKVPALESQVSGSTKCAVFLMSANSEITH-----LVQKRTIDAD 139
 DB ||| ||||| ||||| : : : ||||| ||||| : : : |||
 QY 77 YL-PTGPPPPORDELG-----GPPPTSPALLQCTAERDHDVLSICTLVPRSGEQAE 128
 DB ||| ||||| ||||| : : : ||||| ||||| : : : |||
 QY 140 NQAGLAQCQTGIRKRPATDDSSQNKR 166
 DB ||| ||||| ||||| : : : ||||| ||||| : : : |||
 QY 129 GSPGPGDSQSRKRRTQSMIDFVHSKR 155
 DB ||| ||||| ||||| : : : ||||| ||||| : : : |||
 RESULT 11
 WRK4_ARATH
 ID WRK4_ARATH STANDARD; PRT; 514 AA.
 AC Q9X150; Q93WN8;
 DT 15-JUN-2002 (Pei 41, Created)
 DT 15-JUN-2002 (Pei 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Probable WRKY transcription factor 4 (WRKY DNA-binding protein 4).
 GN WRKY4 OP ATTU1490 OP F7A19.5.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta, Tracheophyta,
 OC Spermatophyta; Magnoliophyta, euembryophytes, core eudicots, Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBL_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chen C., Yu D., Du L., Fan R., Chen Z.;
 RL "Identification of pathogen- and salicylic acid-induced WRKY
 RT DNA-binding activities and genes encoding WRKY DNA-binding proteins in
 RT Arabidopsis".
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia; TISSUE=Flower;
 RA Ulker B., Kushnir S., Somssich I.E.;
 RL "Arabidopsis thaliana transcription factor WRKY4".
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RL MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.P., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altieri D., Araujo P., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk P.F., Chin C.W., Dewar K.,
 RA Chung M.K., Conn L., Conway A.P., Conway A.P., Creasy T.H., Dewar K.,
 RA Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Feng R., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.P., Hughes B., Huizar L.,
 RA Hunter J.F., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam R.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Lueros I.S., Maiti R., Marziani A.,
 RA Millscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pal S., Peterson J., Pham P.K., Rizzo M., Rooney T., Powley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis P.W.;
 RL "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana".
 RL Nature 408:816-820(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.P., Theologis A.;
 RL "KIKEN Arabidopsis full length cDNA clones (RAPUS) sequenced by the
 FT SSP consortium (Salk/Stanford/PGRC)".
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RL -1- SUBCELLULAR LOCATION: "ATH1N_Nuclear (Potential)."

GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd

OM protein - protein search, using sw model

Run on: May 30, 2003, 08:53:57 Search time: 31.2466 seconds
(without alignments)
1181.337 Million cell updates/sec

Title: US-09-865-018b-6

Perfect score: 952

Sequence: 1 MSNVRVNSGSPSLERMDARQ ... DSSPKNKANKIEFNVSVDS 178

Scoring table: BLOSUM62

Gapop 10 0 0, Gapext 0.5

Searched: 671580 seqs, 20604715 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 6%

Maximum Match 100%

Listing first 45 summaries

Database: SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mmc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_protist.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriopl.*
- 17: sp_archaeal.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	910	95.6	198	6 Q9BDC3	Q9BDC3 sus scrofa
2	864	90.8	198	4 Q9NYG6	Q9NYG6 homo sapien
3	864	90.8	198	4 Q9NYG6	Q9NYG6 homo sapien
4	860	90.3	198	4 Q96TE0	Q96TE0 homo sapien
5	840	88.2	197	11 Q08769	Q08769 rattus norv
6	835	87.7	197	11 Q35792	Q35792 rattus norv
7	791	83.1	172	6 Q9EAS5	Q9EAS5 sus scrofa
8	769	80.8	158	4 Q43806	Q43806 homo sapien
9	333	35.0	179	13 Q90YX4	Q90YX4 brachydanio
10	197	20.7	210	13 Q91603	Q91603 xenopus lae
11	193	20.3	209	13 Q91646	Q91646 xenopus lae
12	191.5	20.1	335	11 Q61806	Q61806 mus musculu
13	187	19.6	164	11 Q64315	Q64315 rattus norv
14	168	17.6	42	4 Q9UH60	Q9UH60 homo sapien
15	167.5	17.6	164	4 Q96LE1	Q96LE1 homo sapien
16	161.5	17.0	181	4 Q14010	Q14010 homo sapien

ALIGNMENTS

RESULT 1

Q9BDC3 ID Q9BDC3 PRELIMINARY; PRT; 198 AA.
AC Q9BDC3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE P27K1p1.
GN P27K1p1.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N A
RX MEDLINE=21053196; PubMed=11115398;
FA Hirano K., Hirano M., Zeng Y., Nishimura J., Hara K., Muta K.,
RA Nawata H., Kanai H.;
RT "Cloning and functional expression of a degradation-resistant novel
RT isoform of p27Kip1";
RL Biochem. J. 353:51-57(2001).
DR EMBL; AB031957; BAB39727.1; -;
DR EMBL; AB031955; BAB39725.1; -;
DR EMBL; AB031956; BAB39726.1; -;
DR InterPro; IPR003175; CDI
DR Pfam; PF02234; CDI; 1.
SQ SEQUENCE 198 AA; 22201 MW; E5B01D25E5BDD5F CRC64;

Query Match. 95.6%, Score 910, DB 6, Length 198,
Best local similarity 95.5%, Pred. No. 1.5e-76;
Matches 170; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Q7 1 MSNVRVNSGSPSLERMDARQAEYKESACPNLECFVNHPELTFDLEKHRDMEASQKRW 60
|||||
Q8 1 MSNVRVNSGSPSLERMDARQAEYKESACPNLECFVNHPELTFDLEKHRDMEASQKRW 60
|||||
Q9 61 NFDFQNHKPLEGKYEWQVEKGSPLPEFYFPPPPPPKCAKVPQAESQDVSSTQAVPLMG 120
|||||
10 51 NFDFQNHKPLEGKYEWQVEKGSPLPEFYFPPPPPPKCAKVPQAESQDVSSTQAVPLMG 120

Q9QXHO rattus norv
Q22198 caenorhabdi
Q9H4R1 caenorhabdi
Q22197 caenorhabdi
Q8WQ22 drosophila
Q04154 arabidopsis
Q82809 arabidopsis
P91554 drosophila
Q03973 saccharomyc
Q9VIC8 drosophila
Q9KK24 streptococ
Q94336 drosophila
Q9TNE4 arabidopsis
Q81563 mus musculu
Q91MGI arabidopsis
Q9KK17 streptococ
Q9KK37 streptococ
P91668 drosophila
Q93V92 nicotiana t
Q9QZ47 mus musculu
Q9QW18 mus musculu
Q9QW17 oryza sativ
Q9KK40 streptococ
Q35613 mus musculu
Q9FDQ1 streptococ
Q99VK7 staphylococ
Q91J15 arabidopsis
Q93V23 arabidopsis
Q91S28 pisum sativ


```

10 EEMISAFVAVLPEKLSAGIGAGACPNLPSPHGHGMPSELKPLKEKLEKASLQKWNFFDPEP 69
68 KPLGKGYQWQVKEGKSIPEFYYPDPPEPKACKVAGESULVSQSDTFCGAVLIMDSQANSED 127
70 TPLKGIETWPEVSEKMPSEYQNPSTAAATTSPEQQGQLLVSPQEP--PEEAPVD 126
128 THLYDQKTDADNGLAGLAEQCTRIKPKPPATFSSPQNKRPANP 169
127 VNVNENPCAKFNFAKIVKPKQGVF--GPAFASANISLQPKPK 167

RESULT 14
Q91V06 PRELIMINARY; PRT; 335 AA.
AC Q91V06;
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DI 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Cyclin dependent kinase inhibitor 1C (p57Kip2 protein) (P57).
GN CDKN1C OR p57KIP2.
OS Mus musculus domesticus (western European house mouse), and
Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10097; 10097;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Mus musculus domesticus; STRAIN=129 SV;
RX MEDLINE=20519229; PubMed=11861728;
RA Engelmann S.; Stroedter M.; Paulsen M.; Frank G.; Reinhardt P.;
Lane N.; Reik W.; Walter J.
RT "Sequence and functional comparison in the Beckwith-Wiedemann region:
implications for a novel imprinting centre and extended imprinting."
PL Hum. Mol. Genet. 9:2691-2706(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Mus musculus domesticus; STRAIN=129 SV;
RA Engelmann S.;
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; STRAIN=129/SV;
RX MEDLINE=20014712; PubMed=10545601;
RA John R.M., Hodges M., Little P., Barton S.C., Surani M.A.
RT "A human p57KIP2 transgene is not activated by passage through the
maternal mouse germline."
PL Hum. Mol. Genet. 8:2211-2219(1999)
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; TISSUE=PREAST TUMOR;
RA Strausberg R.;
RX Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
DR EMBL: AJ276505; CAC16402.1;
DR EMBL: AF160190; AAF00984.1;
DR EMBL: BC005412; AAH05412.1;
DR MGD: MGI:104564; Cdkn1c;
DR InterPro: IPR003175; Cbl.
DR P38; P02234; Cbl; 1.
KW Kinase.
SQ SEQUENCE 335 AA; 45003 MW; 450676287FEREF CRG64;

Query Match 20.1%; Score 191.5; DB 11; Length 335;
Best Local Similarity 31.68; Pred. No. 9.2e-10;
Matches 54; Conservative 24; Mismatches 52; Indels 41; Gaps 7;

QY 13 LERPTAGAEYF KFSATENIPSPYVNHFFETFOLEKHEFFMEFASCKWNTFFQNIKE 69
DB 1 MERL-ASSDTPVVIARSSACHSLFGVPVDHDELGRLEMLRLAELNAELDNKWDENFQDVP 59
QY 70 LE--GKYQWQVFKGSIPEFYYP-----PPPKGACKV-----PAGESQVS 110
DB 60 LQVGRPLQWMEVDSVFAEYFETVQVDFPLGLSPFPFPFVAVAVIFRSFPAEAFD-- 117

```

```

QY 111 GTFQAVPLMSQANSETHLVKRTITAINAGSLAPQCTGIPKPKALDSS 161
DB 118 GLEEA-----PEQPPSAPASAVAEPTTPATPAPASDLTS 152

RESULT 13
Q64315 PRELIMINARY; PRT; 164 AA
AC Q64315;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DI 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE P21 (WAF1).
GN WAF1 OR CIP1.
OS Rattus norvegicus (Rat)
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95316868; PubMed=7756420;
RA el-Deiry W.S.; Tokino T.; Waldman T.; Velculescu V.; Oliner J.D.;
Burrell M.; Hill D.E.; Fees J.L.; Hamilton S.F.; Kinzler K.W.;
Vogelstein B.;
RT "Topological control of p21WAF1/CIP1 expression in normal and
neoplastic tissues."
PL Cancer Res. 55:2910-2919(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX SIPAIN=F44/N; TISSUE=LUNG;
RA Belinsky S.A.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
DR EMBL: U24174; AAC5221.1;
DR EMBL: L41275; AAC42084.1;
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; Cdi; 1.
SQ SEQUENCE 164 AA; 18318 MW; 6057E86045E6435F CRG64;

Query Match 19.6%; Score 187; DB 11; Length 164;
Best Local Similarity 26.9%; Pred. No. 9.9e-10;
Matches 43; Conservative 25; Mismatches 66; Indels 26; Gaps 3;

QY 17 DAFQARYPKPSATPNLFGPVNHEELTFPLEKIPRPMEEASQPKWNFDGNHXPLEGKYEW 76
DB 6 EVRPVPH-RSKVCRKLFGVDSEQSPKCDALMASCLQPARGRWNFDATFTPLEGNYVM 64
QY 77 QEVERKSLPEFYYPPEPKGA-KVIAQESQVSGTFQAVPLMSQANSETHLYDQKTD 136
DB 65 FQVPSPLPKVYLSP-----GSKPKPLDGLGPKPPSTSSALIGGPGP 105
QY 137 TAINDAELAEQCTGIRKPPATFSSP-----QNKRPANPT 170
DB 106 APEDHVALSLSQTLVSHAPERPPDPSGDTSGRKRPPOT 145

RESULT 14
Q90H60 PRELIMINARY; PRT; 42 AA.
AC Q90H60;
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DI 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DI 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Cyclin-dependent kinase inhibitor p27 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Walthregny D.; Loda M.;
RT "Homo sapiens cyclin-dependent kinase inhibitor p27 intron."
PL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

```


Genome version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 08:52:12 : Search time 14 718 Seconds
(without alignments)
606.682 Million cell updates/sec

Title: US-09-865-018b-6_copy_22_88

Perfect score: 378
Sequence: 1 EYKPSACPNLEFVNRFEI... PLEKRYEWEVENSLPEFF 57

Scoring table: BLOSUM62

Gapop 10 0 : Gapext 0 5

Searched: 90476 seqs, 13250420 residues

Total number of hits satisfying chosen parameters: 90476

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database : A_Geneset_131002_*
1: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1460.DAT*
2: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1461.DAT*
3: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1462.DAT*
4: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1463.DAT*
5: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1464.DAT*
6: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1465.DAT*
7: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1466.DAT*
8: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1467.DAT*
9: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1468.DAT*
10: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1469.DAT*
11: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1470.DAT*
12: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1471.DAT*
13: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1472.DAT*
14: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1473.DAT*
15: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1474.DAT*
16: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1475.DAT*
17: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1476.DAT*
18: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1477.DAT*
19: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1478.DAT*
20: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1479.DAT*
21: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1480.DAT*
22: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1481.DAT*
23: /SIDS2/qcadata/geneseq/geneseq-emb1/AA1482.DAT*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	378	100.0	178	AA179131	Mink kipl, p27-kipl
2	378	100.0	178	AA179131	Mink p27 kipl part
3	378	100.0	178	AA179131	Partial 27 kda pro
4	370	97.9	172	AA151588	Porcine p27kipl po
5	370	97.9	172	AA151589	Porcine p27kipl po
6	360	95.2	167	AA195101	Truncated p27 prot
7	360	95.2	177	AA197530	Truncated human p2
8	360	95.2	177	AA196072	Human truncated cy
9	360	95.2	177	AA196072	Human cyclin depen
10	360	95.2	194	AA194930	Amino acid sequenc

11	360	95.2	198	AA179133	Human kipl, p27-ki
12	360	95.2	198	AA179133	Human p27 kipl. H
13	360	95.2	198	AA179133	27 kda protein inh
14	360	95.2	198	AA179133	Amino acid sequenc
15	360	95.2	198	AA179133	CKI/KIP protein p2
16	360	95.2	198	AA179133	Human p27 protein
17	360	95.2	198	AA179133	Human cyclin depen
18	360	95.2	198	AA179133	Human cyclin depen
19	360	95.2	198	AA179133	Human mutant cycli
20	360	95.2	198	AA179133	Human p27(kipl) ki
21	360	95.2	198	AA179133	Amino acid sequenc
22	360	95.2	198	AA179133	Human p27 protein
23	360	95.2	198	AA179133	Human p27 protein
24	360	95.2	198	AA179133	Truncated p27/p16
25	360	95.2	198	AA179133	Human W8 protein s
26	360	95.2	198	AA179133	Antiproliferative
27	360	95.2	198	AA179133	Angiogenesis inhib
28	360	95.2	198	AA179133	Truncated p27/p16
29	360	95.2	198	AA179133	Human W7 protein s
30	360	95.2	198	AA179133	Antiproliferative
31	360	95.2	198	AA179133	Angiogenesis inhib
32	360	95.2	198	AA179133	CDK inhibitor fus
33	360	95.2	198	AA179133	Human p16p27 fusio
34	360	95.2	198	AA179133	Human W4 protein s
35	360	95.2	198	AA179133	Human W6 protein s
36	360	95.2	198	AA179133	Antiproliferative
37	360	95.2	198	AA179133	Angiogenesis inhib
38	360	95.2	198	AA179133	Antiproliferative
39	360	95.2	198	AA179133	Angiogenesis inhib
40	360	95.2	198	AA179133	CDK inhibitory fus
41	360	95.2	198	AA179133	Human p16(OS)p27 f
42	360	95.2	198	AA179133	Human W5 protein s
43	360	95.2	198	AA179133	Antiproliferative
44	360	95.2	198	AA179133	Angiogenesis inhib
45	360	95.2	198	AA179133	Angiogenesis inhib

ALIGNMENTS

RESULT 1					
AA179131	AA179131 standard; protein, 178 AA.				
AC	AA179131:				
DT	27-FEB-1996 (first entry)				
DE	Mink kipl, p27-kipl or p27, cyclin E-Cdk2 activation inhibitor.				
XX	Mink kipl, p27-kipl, p27, cyclin E-Cdk2 complex, cancer;				
KW	activation inhibitor, hyperplasia; cyclin dependent kinase;				
KW	diagnosis, hyperproliferative disorder; ulcer; partial protein.				
XX	Mustela vison.				
OS	Mustela vison.				
XX	Key	Location/Qualifiers			
FT	Peptide	31..43			
FT		/note= "obtd. from purified kipl, and			
FT		used to design degenerate oligo-			
FT		nucleotide PCR primer"			
FT	Peptide	74..79			
FT		/note= "obtd. from purified kipl, and			
FT		used to design degenerate oligo-			
FT		nucleotide PCR primer"			
FT	Peptide	83..96			
FT		/note= "obtd. from purified kipl"			
FT	Peptide	114..123			
FT		/note= "obtd. from purified kipl"			
FT	Peptide	135..147			
FT		/note= "obtd. from purified kipl"			
XX					
PN	W09518824-A1.				

PT especially breast carcinoma
XX
PS Disclosure; Fig 13b; 105pp; English.
XX
CC The present sequence represents a partial 27 kDa protein (p27 or Kip1)
CC which inhibits the activation of a cyclin E-cyclin-dependent kinase2
CC (Cdk2) complex. A reduced relative level of kip1 is indicative of a
CC hyperproliferative disease (particularly cancer, especially breast
CC carcinoma) and also is prognostic for increased risk of death and/or
CC recurrence of cancer (and may be used to determine suitable treatments).
CC Agents that affect the activity of kip1 can be used to treat
CC hyperproliferative conditions, e.g. to stimulate tissue or organ repair
CC or to establish cell cultures.

XX
SQ Sequence 178 AA;

Query Match 100.0%; Score 378; DB 19; Length 178;
Best Local Similarity 100.0%; Pred. No. 4.3e-41;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYKPSACRNLFQPVNHEELTRLEKHRRDMEASQKWNFDQNHKPLEGKYEWQVEK 60
DB 22 EYKPSACRNLFQPVNHEELTRLEKHRRDMEASQKWNFDQNHKPLEGKYEWQVEK 81
QY 61 GSLPEFY 67
DB 82 GSLPEFY 88

RESULT 4

AAM51588
ID AAM51588 standard; Protein; 172 AA.

XX
AC AAM51588;

DT 01-FEB-2002 (first entry)

XX Porcine p27Kip1 polypeptide #1.

XX Pig, antiarteriosclerotic; cytostatic; gene therapy; p27Kip1;
KW proteasome decomposition resistance; cancer; arteriosclerosis.

XX
OS Sus scrofa.

PN JP2001258561-A

XX
PD 25-SEP-2001.

XX 17-MAR-2000; 2000JP-0076840.

XX 17-MAR-2000; 2000JP-0076840.

XX (UYKY-) UNIV KYUSHU.

XX WPI; 2002-003329/01

DR N-PSDB; ABA01079.

XX Nucleic acid and amino acid sequence for showing resistance against
PT proteasome decomposition, comprises a new p27Kip1 molecular species -

XX
PS Disclosure; Page 6-7; 12pp; Japanese.

XX The invention relates to a novel p27Kip1 polynucleotide and protein
CC The p27Kip1 protein shows resistance to proteasome decomposition
CC and can be used in the treatment of cancers and arteriosclerosis. The
CC invention also relates to a recombinant vector containing the
CC polynucleotide, and to a transformant containing the recombinant
CC vector. The present sequence is the polypeptide of the invention.

XX
SQ Sequence 172 AA;

Query Match 97.9%; Score 370; DB 23; Length 172;
Best Local Similarity 98.5%; Pred. No. 4.5e-40;

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EYKPSACRNLFQPVNHEELTRLEKHRRDMEASQKWNFDQNHKPLEGKYEWQVEK 60
DB 14 EYKPSACRNLFQPVNHEELTRLEKHRRDMEASQKWNFDQNHKPLEGKYEWQVEK 73
QY 61 GSLPEFY 67
DB 74 GSLPEFY 80

RESULT 5

AAM51589
ID AAM51589 standard; Protein; 198 AA.

XX
AC AAM51589;

DT 01-FEB-2002 (first entry)

XX Porcine p27Kip1 polypeptide #2.

XX Pig; antiarteriosclerotic; cytostatic; gene therapy; p27Kip1;
KW proteasome decomposition resistance; cancer; arteriosclerosis.

XX
OS Sus scrofa.

PN JP2001258561-A.

XX
PD 25-SEP-2001.

XX 17-MAR-2000; 2000JP-0076840.

XX 17-MAR-2000; 2000JP-0076840.

XX (UYKY-) UNIV KYUSHU.

DR WPI; 2002-003329/01.

DR N-PSDB; ABA01080.

XX Nucleic acid and amino acid sequence for showing resistance against
PT proteasome decomposition, comprises a new p27Kip1 molecular species -

XX
PS Disclosure; Page 8-9; 12pp; Japanese.

XX The invention relates to a novel p27Kip1 polynucleotide and protein
CC The p27Kip1 protein shows resistance to proteasome decomposition
CC and can be used in the treatment of cancers and arteriosclerosis. The
CC invention also relates to a recombinant vector containing the
CC polynucleotide, and to a transformant containing the recombinant
CC vector. The present sequence is a p27Kip1 polypeptide.

XX
SQ Sequence 198 AA;

Query Match 97.9%; Score 370; DB 23; Length 198;
Best Local Similarity 98.5%; Pred. No. 5.4e-40;

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKPSACRNLFQPVNHEELTRLEKHRRDMEASQKWNFDQNHKPLEGKYEWQVEK 60
DB 22 EYKPSACRNLFQPVNHEELTRLEKHRRDMEASQKWNFDQNHKPLEGKYEWQVEK 81

QY 61 GSLPEFY 67

DB 82 GSLPEFY 88

RESULT 6

AAW95101
ID AAW95101 standard; Protein; 167 AA.

XX
AC AAW95101;

DT 25-MAY-1999 (first entry)

OS Synthetic.
 XX Key Location/Qualifiers
 FH Peptide 1..11
 FT /label= Haemagglutinin epitope
 FT Protein 12..177
 XX /label= p27(12-178)

PN WC200052158-A1.

XX 08-SEP-2000.

XX 28-FEB-2000; 2000W0-US04971.

XX 01-MAR-1999; 990S-0122974.

XX 05-NOV-1999; 990S-0163692.

XX 09-DEC-1999; 990S-0457568.

XX (CELL-) CELL GENESYS INC.

XX (MITO-) MITOTIX INC.

XX McArthur J, Gyuris J, Finan M;

XX WPI: 2000-544183/56

XX N-PSDB: AAA50492.

XX Novel recombinant lentivirus for inhibiting proliferation of smooth

XX muscle cells in e.g. testis, is replication deficient and comprises

XX a transgene encoding a cyclin dependent kinase inhibitor

XX Example 1, Page 109-110, 126pp, English.

XX The present sequence is that of truncated human p27 protein in

XX which the first 12 N-terminal and the final 21 C-terminal amino

XX acids of full-length p27 (see AAY96066) are deleted to remove a CDK

XX consensus phosphorylation site at amino acids 187-190, a potential

XX phosphorylation site for proline-directed kinases at amino acids

XX 178-181 and a weak CDK phosphorylation site at amino acids 10-13.

XX p27 is a cyclin dependent kinase inhibitor (CDKi). A claimed

XX method for inhibiting smooth muscle cell hyperproliferation involves

XX transducing smooth muscle cells with a replication-deficient

XX recombinant adenovirus that lacks a functional E1 region and a

XX functional E4 region, and comprises a transgene encoding a CDKi.

XX The CDKi is an INK4 family protein such as human p16, a CIP/KIP

XX family protein such as p27, active fragments of these, e.g.

XX p27(12-178aa), or fusion proteins comprising (active fragments of)

XX an INK4 family protein and a CIP/KIP family protein (see AAY96046 and

XX AAY96049). The method is used to inhibit mammalian smooth muscle

XX cell hyperproliferation induced by injury caused by angioplasty,

XX stent placement or vein grafting. It is useful for treating

XX vascular pathologies, e.g. restenosis. Also claimed are recombinant

XX lentiviruses encoding CDKis. Use of truncated p27 was designed to

XX increase the protein's half-life and to eliminate potential

XX phosphorylation sites involved in the negative regulation of CDKi

XX activity.

XX Sequence 177 AA.

XX Query Match 95.2%; Score 360; DB 21; Length 177;

XX Best Local Similarity 95.5%; Prod No 9 4e-30;

XX Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

XX 1 EYFYSAGNLRPGVNNHETLTCLEKHEHMEESQPKWNEFVNHKPLSKYQWEK 60

XX 22 EFKETSAKRLFGFVZHEELINLEKRGKRWFEASLKKWNECFVNHKPLSKYQWEK 81

XX 61 GSLPEFY 67

XX 82 GSLPEFY 88

XX RESULT 9

XX AAY96072

ID XX AAY96072 standard; Protein; 177 AA.
 AC XX AAY96072;
 DI 05-DEC-2000 (first entry)
 XX Human cyclin dependent kinase inhibitor p27(12-178).
 DE
 XX Cyclin dependent kinase inhibitor; CDKi; CIP; KIP; human; p27;
 KW angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;
 KW endometriosis; psoriasis; vascular retinopathy; cytostatic;
 KW antiarthritic; antirheumatic; gynaecological; antipsoriatic;
 KW antiproliferative; gene therapy; mutant; mutein.
 XX Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Peptide 1..11
 FT /label= Haemagglutinin-epitope
 FT Protein 12..177
 FT /label= p27(12-178)
 XX WC200052158-A1.
 XX 08-SEP-2000.
 XX 28-FEB-2000; 2000W0-US04970.
 XX 01-MAR-1999; 990S-0122974.
 XX 05-NOV-1999; 990S-0163692.
 XX 09-DEC-1999; 990S-0457646.
 XX (CELL-) CELL GENESYS INC.
 XX (MITO-) MITOTIX INC.
 XX Patel S, McArthur J, Gyuris J;
 XX WPI: 2000-5445501/52.
 XX N-PSDB: AAA50527.
 XX Inhibiting angiogenesis and treating angiogenesis-associated
 XX conditions, e.g. neoplasia, psoriasis by transducing an endothelial
 XX cell with a recombinant virus having a transgene encoding a cyclin
 XX dependent kinase inhibitor
 XX Example 1; Page 117-118; 138pp; English.
 XX The present sequence is that of a truncated human p27 protein in
 XX which the first 12 N-terminal and the final 21 C-terminal amino
 XX acids of full-length p27 (see AAY96066) are deleted to remove a CDK
 XX consensus phosphorylation site at amino acids 187-190, a potential
 XX phosphorylation site for proline-directed kinases at amino acids
 XX 178-181 and a weak CDK phosphorylation site at amino acids 10-13.
 XX p27 is a cyclin dependent kinase inhibitor (CDKi) that inhibits
 XX angiogenesis. A claimed method for inhibiting angiogenesis
 XX involves transducing an epithelial cell with a transgene encoding
 XX (internalizable, secretable) CDKi. The delivery system for the
 XX transgene may be a liposome or a recombinant virus. The CDKi is
 XX a protein of the CIP/KIP family such as p27, a protein of the
 XX INK4 family such as p16, active fragments of these proteins (e.g.
 XX amino acids 25-93 or 12-178 of human p27), or a fusion protein
 XX comprising 2 CDKi proteins such as (truncated) p27 and p16 (see
 XX AAY96068-80). The method is used to treat conditions associated with
 XX angiogenesis, e.g. neoplasia, rheumatoid arthritis, endometriosis,
 XX psoriasis and vascular retinopathy (claimed). Alternatively, the
 XX transgene is delivered to an auxiliary cell, and is expressed by
 XX that cell such that the CDKi is released into the blood and
 XX targets the target epithelial cell. Use of truncated p27 was
 XX designed to increase the protein's half-life and to eliminate
 XX potential phosphorylation sites involved in the negative
 XX regulation of CDKi activity.

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd

OM protein protein search, using sw model

Run on: May 30, 2003, 08:55:37 : Search time 5.02067 seconds
(without alignments)
392.644 Million cell updates/sec

Title: US-09-865-018b-6_copy_22_88
Perfect score: 378
Sequence: 1 EYPKPSACPNLF:PVNHEEL PLECKYPMQVFPKLSLPEFY 67

Scoring table: BLOSUM62
Gapop 10 0 0 Gapext 0 5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA*
1: /seq2.6/ptdata/1/iaa/CA/CA.MR.rep.*
2: /seq2.6/ptdata/1/iaa/CA/CA.MR.rep.*
3: /seq2.6/ptdata/1/iaa/CA/CA.MR.rep.*
4: /seq2.6/ptdata/1/iaa/CA/CA.MR.rep.*
5: /seq2.6/ptdata/1/iaa/CA/CA.MR.rep.*
6: /seq2.6/ptdata/1/iaa/CA/CA.MR.rep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	378	100.0	178	4	US-08-794-002-6
2	378	100.0	178	4	US-08-854-039B-6
3	378	100.0	198	1	US-08-275-983B-1
4	378	100.0	198	1	US-08-794-002-2
5	360	95.2	177	4	US-03-457-568-12
6	360	95.2	177	4	US-09-457-568-12
7	360	95.2	198	1	US-08-406-248-4
8	360	95.2	198	1	US-08-897-333A-2
9	360	95.2	198	4	US-08-240-068-2
10	360	95.2	198	4	US-08-794-002-2
11	360	95.2	198	4	US-09-457-568-12
12	360	95.2	198	4	US-09-457-568-12
13	360	95.2	334	4	US-09-457-568-16
14	360	95.2	334	4	US-09-457-568-16
15	360	95.2	334	4	US-09-457-568-16
16	360	95.2	348	4	US-09-457-568-14
17	360	95.2	348	4	US-09-457-568-14
18	360	95.2	365	4	US-09-457-568-10
19	360	95.2	365	4	US-09-457-568-10
20	360	95.2	365	4	US-09-457-568-10
21	360	95.2	365	4	US-09-457-568-10
22	360	95.2	380	4	US-09-457-568-8
23	360	95.2	380	4	US-09-457-568-8
24	360	95.2	391	1	US-08-589-981-2
25	360	95.2	391	4	US-09-457-568-4
26	360	95.2	391	4	US-09-457-568-4
27	357	94.4	198	4	US-08-854-039B-2

Sequence 2, Appli
Sequence 8, Appli
Sequence 57, Appli
Sequence 4, Appli
Sequence 18, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 6, Appli
Sequence 30, Appli
Sequence 56, Appli
Sequence 50, Appli
Sequence 53, Appli
Sequence 52, Appli
Sequence 49, Appli

ALIGNMENTS

RESULT 1
US-08-794-002-6
Sequence 6, Application US/08794002
Patent No. 6316208
GENERAL INFORMATION:
APPLICANT: Roberts, James M.
APPLICANT: Porter, Peggy L.
TITLE OF INVENTION: ISOLATED P-2 PROTEIN AND METHODS FOR ITS
TITLE OF INVENTION: PRODUCTION AND USE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,002
FILING DATE: 03-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-079, 03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1009
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-794-002-6

Query Match: 100.0% Score: 378 DB: 4 Length: 178
Best Local Similarity: 100.0% P-2 N: 1.7e-41
Matches: 67 Conservative: 0 Mismatches: 0 Indels: 0 Gaps: 0
Query 1 EYPKPSACPNLF:PVNHEEL PLECKYPMQVFPKLSLPEFY 67
DB 22 EYPKPSACPNLF:PVNHEEL PLECKYPMQVFPKLSLPEFY 67
Query 61 GSLPEFY 67

REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: M1-079,03
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 22
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-794-002-22

Query Match 100.0% Score 378; DB 4; Length 198,
Best Local Similarity 100.0%; Pred. No. 1.9e-41;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EYPKPSACNLFGPVNHEELTRDLEKRRDMEESQRKNWDFONHKPLEGKYEWQVEK 60
Db |||||||
22 EYPKPSACNLFGPVNHEELTRDLEKRRDMEESQRKNWDFONHKPLEGKYEWQVEK 81
QY 61 GSLPEFY 67
Db ||||||| 82 GSLPEFY 88

RESULT 5
US-09-457-568-12
Sequence 12, Application US/09457568
Patent No. 6413943
GENERAL INFORMATION:
APPLICANT: McArthur, James G
APPLICANT: Gyuris, Jen
APPLICANT: Finer, Mitchell H
TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
TITLE OF INVENTION: Smooth Muscle Cells
FILE REFERENCE: 106482.691
CURRENT APPLICATION NUMBER: US/09/457-568
EARLIER FILING DATE: 1999-12-09
EARLIER APPLICATION NUMBER: 60/122-974
EARLIER FILING DATE: 1999-03-01
EARLIER APPLICATION NUMBER: 60/163,682
EARLIER FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 12
LENGTH: 177
TYPE: PRT
ORGANISM: Homo sapiens
US-09-457-568-12

Query Match 95.2% Score 360; DB 4; Length 177;
Best Local Similarity 95.5%; Pred. No. 3.7e-39;
Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0,
QY 1 EYPKPSACNLFGPVNHEELTRDLEKRRDMEESQRKNWDFONHKPLEGKYEWQVEK 60
Db |||||||
22 EYPKPSACNLFGPVNHEELTRDLEKRRDMEESQRKNWDFONHKPLEGKYEWQVEK 81
QY 61 GSLPEFY 67
Db ||||||| 82 GSLPEFY 88

RESULT 6
US-09-457-646-12
Sequence 12, Application US/09457646
Patent No. 6420345
GENERAL INFORMATION:
APPLICANT: Patel, Salil D
APPLICANT: McArthur, James G
APPLICANT: Gyuris, Jen

TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
TITLE OF INVENTION: Smooth Muscle Cells
FILE REFERENCE: 106482.287
CURRENT APPLICATION NUMBER: US/09/457,646
EARLIER FILING DATE: 1999-12-09
EARLIER APPLICATION NUMBER: 60/122,974
EARLIER FILING DATE: 1999-03-01
EARLIER APPLICATION NUMBER: 60/163,682
EARLIER FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 12
LENGTH: 177
TYPE: PRT
ORGANISM: Homo sapiens
US-09-457-646-12

Query Match 95.2% Score 360; DB 4; Length 177,
Best Local Similarity 95.5%; Pred. No. 3.7e-39;
Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EYPKPSACNLFGPVNHEELTRDLEKRRDMEESQRKNWDFONHKPLEGKYEWQVEK 60
Db |||||||
22 EYPKPSACNLFGPVNHEELTRDLEKRRDMEESQRKNWDFONHKPLEGKYEWQVEK 81
QY 61 GSLPEFY 67
Db ||||||| 82 GSLPEFY 88

RESULT 7
US-08-275-983B-3
Sequence 3, Application US/08275983B
Patent No. 5688665
GENERAL INFORMATION:
APPLICANT: Massague, Joan
APPLICANT: Roberts, James M.
APPLICANT: Koff, Andrew
APPLICANT: Polyak, Kornelia
TITLE OF INVENTION: Isolated p27 protein, Nucleic Acid Molecules
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/275,983B
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/179,045
FILING DATE: 07-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: M1-079CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
Encoding


```

; TITLE OF INVENTION: PRODUCTION AND USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,002
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-079,03
; TELEPHONE: 617-832-1000
; TELEFAX: 617-842-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-794-002-2

Query Match 95.2%; Score 360; DB 4; Length 198;
Best Local Similarity 95.5%; Pred. No. 4.2e-39;
Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKPSACRNLFPGVNVNHEELTRDLEKHRTMFEEASQKWNFDQNHKPLEGKYEQVEK 60
   1:|||||
Db 22 EHPKSACRNLFPGVDHEELTRDLEKHCRDMEASQKWNFDQNHKPLEGKYEQVEK 81
   1:|||||

QY 61 GSLPEFY 67
   |||||
Db 82 GSLPEFY 88

RESULT 12
US-09-457-568-26
; Sequence 26, Application US/09457568
; Patent No. 6413943
; GENERAL INFORMATION:
; APPLICANT: McArthur, James G
; APPLICANT: Gyuris, Jenö
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
; FILE REFERENCE: 106482.691
; CURRENT APPLICATION NUMBER: US/09/457,568
; CURRENT FILING DATE: 1999-12-09
; EARLIER APPLICATION NUMBER: 60/122,974
; EARLIER FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 60/163,682
; EARLIER FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-568-26

Query Match 95.2%; Score 360; DB 4; Length 198;
Best Local Similarity 95.5%; Pred. No. 4.2e-39;
Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKPSACRNLFPGVNVNHEELTRDLEKHRTMFEEASQKWNFDQNHKPLEGKYEQVEK 60
   1:|||||
Db 22 EHPKSACRNLFPGVDHEELTRDLEKHCRDMEASQKWNFDQNHKPLEGKYEQVEK 81
   1:|||||

QY 61 GSLPEFY 67
   |||||
Db 82 GSLPEFY 88

RESULT 13
US-09-457-646-26
; Sequence 26, Application US/09457646
; Patent No. 6420345
; GENERAL INFORMATION:
; APPLICANT: Patel, Salil D
; APPLICANT: McArthur, James G
; APPLICANT: Gyuris, Jenö
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
; FILE REFERENCE: 106482.287
; CURRENT APPLICATION NUMBER: US/09/457,646
; CURRENT FILING DATE: 1999-12-09
; EARLIER APPLICATION NUMBER: 60/122,974
; EARLIER FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 60/163,682
; EARLIER FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-646-26

Query Match 95.2%; Score 360; DB 4; Length 198;
Best Local Similarity 95.5%; Pred. No. 4.2e-39;
Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKPSACRNLFPGVNVNHEELTRDLEKHRTMFEEASQKWNFDQNHKPLEGKYEQVEK 60
   1:|||||
Db 22 EHPKSACRNLFPGVDHEELTRDLEKHCRDMEASQKWNFDQNHKPLEGKYEQVEK 81
   1:|||||

QY 61 GSLPEFY 67
   |||||
Db 82 GSLPEFY 88

RESULT 14
US-09-457-568-16
; Sequence 16, Application US/09457568
; Patent No. 6413943
; GENERAL INFORMATION:
; APPLICANT: McArthur, James G
; APPLICANT: Gyuris, Jenö
; APPLICANT: Finer, Mitchell H
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
; FILE REFERENCE: 106482.691
; CURRENT APPLICATION NUMBER: US/09/457,568
; CURRENT FILING DATE: 1999-12-09
; EARLIER APPLICATION NUMBER: 60/122,974
; EARLIER FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 60/163,682
; EARLIER FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-568-16

Query Match 95.2%; Score 360; DB 4; Length 198;
Best Local Similarity 95.5%; Pred. No. 4.2e-39;
Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKPSACRNLFPGVNVNHEELTRDLEKHRTMFEEASQKWNFDQNHKPLEGKYEQVEK 60
   1:|||||
Db 22 EHPKSACRNLFPGVDHEELTRDLEKHCRDMEASQKWNFDQNHKPLEGKYEQVEK 81
   1:|||||

QY 61 GSLPEFY 67
   |||||
Db 82 GSLPEFY 88

RESULT 15
US-09-457-568-16
; Sequence 16, Application US/09457568
; Patent No. 6413943
; GENERAL INFORMATION:
; APPLICANT: McArthur, James G
; APPLICANT: Gyuris, Jenö
; APPLICANT: Finer, Mitchell H
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Proliferation of
; FILE REFERENCE: 106482.691
; CURRENT APPLICATION NUMBER: US/09/457,568
; CURRENT FILING DATE: 1999-12-09
; EARLIER APPLICATION NUMBER: 60/122,974
; EARLIER FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 60/163,682
; EARLIER FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-568-16
```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 Computer Ltd.

OM protein protein search, using sw model

Run on: May 30, 2003, 02:58:52 Search time 5.8395 Seconds
(without alignments)
991.736 Million col: updates/sec

Title: us-09-865-018b-6_copy_22_88

Perfect score: 478

Sequence: 1 EYKPSACPNIFGVNHEFI

Scoring table: BLOSUM62 Gapop 10 0 Gapext 0 5 PILEUPWCEVEKRS[PEFY 67

Searched: 383516 seqs, 101223644 residues 383519

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published_Applications_AA:*

- 1: /cgn2_6/prodata/1/pubpaa/us08_NEW_PUB.pep.*
- 2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
- 14: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	378	100	0	178	10 US-09-865-018b-6
2	369	95	2	167	8 US-08-902-572-18
3	360	95	2	168	9 US-09-970-561-2
4	360	95	2	334	8 US-08-902-572-22
5	360	95	2	348	8 US-08-902-572-24
6	360	95	2	365	8 US-08-902-572-8
7	360	95	2	380	8 US-08-902-572-6
8	360	95	2	391	8 US-08-902-572-2
9	357	94	2	198	10 US-09-865-018b-2
10	356	94	2	197	10 US-09-865-018b-4
11	354	93	7	237	8 US-08-902-572-26
12	354	93	7	252	8 US-08-902-572-28
13	346	91	5	70	8 US-08-902-572-20
14	148	39	2	164	9 US-09-221-268-4
15	148	39	2	164	9 US-09-221-268-5
16	148	39	2	164	10 US-09-865-018b-24
17	148	39	2	164	10 US-09-940-766-2
18	145	38	4	247	10 US-09-925-297-770
19	100	26	5	191	10 US-09-733-507-2

20	100	26	5	191	10	US-09-733-507-10	Sequence 10, Appl
21	81.5	21.6	21.5	215	10	US-09-733-507-12	Sequence 12, Appl
22	81	21.4	137	10	US-09-733-507-14	Sequence 14, Appl	
23	71.5	18.9	196	10	US-09-733-507-16	Sequence 16, Appl	
24	71	18.8	13	10	US-09-865-018-26	Sequence 26, Appl	
25	71	18.8	208	10	US-09-733-507-13	Sequence 13, Appl	
26	67.5	17.9	176	10	US-09-733-507-11	Sequence 11, Appl	
27	66.5	17.6	190	9	US-09-993-308-4	Sequence 4, Appl	
28	66	17.5	13	10	US-09-865-018-27	Sequence 27, Appl	
29	65.5	17.3	147	9	US-10-219-220-173	Sequence 173, App	
30	65	17.2	746	9	US-10-153-668-232	Sequence 232, App	
31	61	16.1	282	9	US-09-845-713A-2	Sequence 2, Appl	
32	60.5	16.0	373	9	US-10-219-220-285	Sequence 285, App	
33	60.5	16.0	396	9	US-10-219-220-153	Sequence 153, App	
34	60	15.9	317	9	US-09-925-299-853	Sequence 853, App	
35	60	15.9	317	10	US-09-925-299-853	Sequence 853, App	
36	60	15.9	552	9	US-09-819-142-22	Sequence 22, Appl	
37	60	15.9	770	9	US-10-153-668-7	Sequence 7, Appl	
38	60	15.7	770	9	US-10-153-668-452	Sequence 452, App	
39	59.5	15.7	1267	9	US-10-059-585-56	Sequence 56, Appl	
40	59	15.6	764	9	US-09-854-133-67	Sequence 67, Appl	
41	59	15.6	764	10	US-09-738-973-67	Sequence 67, Appl	
42	59	15.6	934	9	US-10-072-036-137	Sequence 137, App	
43	59	15.2	933	9	US-10-072-036-135	Sequence 135, App	
44	58	15.2	267	9	US-09-903-308-2	Sequence 2, Appl	
45	58.5	15.5	474	10	US-09-529-063-40	Sequence 40, Appl	

ALIGNMENTS

RESULT 1

US-09-865-018-6

: Sequence b, Application US/09865018

: Patent No. US20020110886A1

: GENERAL INFORMATION:

: APPLICANT: Massague, Joan

: Roberts, James M.

: Koff, Andrew

: Polyak, Kornelia

: TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS

: IDENTIFICATION AND USE

: NUMBER OF SEQUENCES: 27

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: FOLEY, HOAG & ELIOT LLP

: STREET: One Post Office Square

: CITY: Boston

: STATE: MA

: COUNTRY: USA

: ZIP: 02109-2170

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patent In Release #1.0, Version #1.30

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/09/865,018

: FILING DATE: 24-May-2001

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US/08/854,039

: FILING DATE: 09-MAY-1997

: ATTORNEY/AGENT INFORMATION

: NAME: Vincent, Matthew P.

: REGISTRATION NUMBER: 36,709

: REFERENCE/DOCKET NUMBER: MIV-079.04

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 617-832-1000

: TELEFAX: 617-832-7090

: INFORMATION FOR SEQ ID NO: 6

: SEQUENCE CHARACTERISTICS:

: LENGTH: 178 amino acids

: TYPE: amino acid

: TOPOLOGY: linear

Db 22 EYKPSACNLPQVDPVHEELTRDLKKHCRDMEASQRKWNFDQNHKPLEGKYEWQVEVK 81

QY 61 GSLPEFY 67

Db 82 GSLPEFY 88

RESULT 10

US-09-865-018-4

; Sequence 4, Application US/09865018

; Patent No. US20026068706A1

; GENERAL INFORMATION:

; APPLICANT: Massague, Joan

; Kofl, Andrew

; Polyak, Kornelia

; TITLE OF INVENTION: INTEGRATED p27 PROTEIN AND METHOD FOR ITS

; PRODUCTION AND USE

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109-2170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; FILING DATE: 24-May-2001

; PRIORITY APPLICATION DATA:

; FILING DATE: 09-MAY-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: MIV-074,04

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-832-1000

; TELEFAX: 617-832-7000

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 197 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-865-018-4

Query Match, 94.2%, Score 356, DB 10, Length 197;

Best local Similarity 92.5%, Pred. No. 2.9e-34;

Matches 62; Conservative 4; Mismatches 1; Indels 0, Gaps 0,

QY 1 EYKPSACNLPQVDPVHEELTRDLKKHCRDMEASQRKWNFDQNHKPLEGKYEWQVEVK 60

Db 22 EYKPSACNLPQVDPVHEELTRDLKKHCRDMEASQRKWNFDQNHKPLEGKYEWQVEVK 81

QY 61 GSLPEFY 67

Db 82 GSLPEFY 88

RESULT 11

US-08-902-572-28

; Sequence 26, Application US/08902572

; Patent No. US20026068706A1

; GENERAL INFORMATION:

; APPLICANT: Gyuris, Jeno

; APPLICANT: Lamphere, Lou

; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND

; RELATED THERETO

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109-2170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICANT: Beach, David H.

; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND

; RELATED THERETO

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109-2170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/902,572

; FILING DATE: 29-JUL-1997

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: MIV-069,03

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-832-1000

; TELEFAX: 617-832-7000

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 237 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-902-572-26

Query Match, 93.7%, Score 354, DB 8, Length 237,

Best local Similarity 94.0%, Pred. No. 6.1e-34;

Matches 63; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EYKPSACNLPQVDPVHEELTRDLKKHCRDMEASQRKWNFDQNHKPLEGKYEWQVEVK 60

Db 9 EYKPSACNLPQVDPVHEELTRDLKKHCRDMEASQRKWNFDQNHKPLEGKYEWQVEVK 68

QY 61 GSLPEFY 67

Db 69 GSLPEFY 75

RESULT 12

US-08-902-572-28

; Sequence 28, Application US/08902572

; Patent No. US20026068706A1

; GENERAL INFORMATION:

; APPLICANT: Gyuris, Jeno

; APPLICANT: Lamphere, Lou

; APPLICANT: Beach, David H.

; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND

; RELATED THERETO

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109-2170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

Query Match 39.28, Score 148, DB 9, Length 164;
Best Local Similarity 42.68, Pred. No. 6.5e-10;
Matches 26, Conserved 11, Mismatches 24, Indels 0, Gaps 0,
QY 7 ACNLEGEVNHETIRGLEKERRDMFFASGEKWNLEFCGNHKPIFGKYEWQVEVEKGSLLPER 66
DB 17 ACNLEGEVNHETIRGLEKERRDMFFASGEKWNLEFCGNHKPIFGKYEWQVEVEKGSLLPER 66
QY 67 Y 67
DB 77 Y 77

Search completed: May 30, 2003, 09:05:12
Job time : 6.8385 secs

Genome version 5.1.6
Copyright (c) 1993 - 2003 Computer Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 08:54:42 - Search time 5.6262 seconds
(without alignments)
1144.739 Million cell updates/sec

Title: US-09-865-018b-6_copy_22_88

Perfect score: 378
Sequence: 1 EYKPSACPNLFQVNHDEL PLEKYEWEVEKSLPEFY 67

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 9%
Maximum Match 100%
Listing first 45 summaries

Database: PIR73:★
1: pir1:★
2: pir2:★
3: pir3:★
4: pir4:★

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	357	94.4	198	2 152718	gene p27kip1 prote
2	356	94.2	197	2 149064	cyclin-cdk inhibit
3	176	46.6	316	2 002424	cyclin-dependent k
4	172	45.5	210	2 151683	cyclin-dependent k
5	168	44.4	348	2 149262	cyclin-cdk inhibit
6	155	41.0	164	2 184725	tumor suppressor p
7	148	39.2	181	2 168674	cyclin-dependent k
8	146	38.6	181	2 154480	cyclin-dependent k
9	141	37.3	159	2 149023	tumor suppressor p
10	138	36.5	143	2 A49438	p53 tumor suppress
11	115.5	30.6	258	2 T24499	hypothetical prote
12	100	26.5	191	2 T81132	cyclin-dependent k
13	87.5	23.1	184	2 T24366	hypothetical prote
14	74.5	19.7	470	2 S00883	phosphatase - short
15	73.5	19.4	489	2 S63401	hypothetical prote
16	71.5	18.9	195	2 H96532	hypothetical prote
17	71.5	18.9	196	2 T09968	cyclin-dependent k
18	69.5	18.4	533	2 S52046	deoxyribodipyrimid
19	69	18.3	279	2 T26166	hypothetical prote
20	67.5	17.9	209	2 T46149	hypothetical prote
21	67.5	17.9	246	1 S49770	hypothetical prote
22	67	17.7	120	2 ARL425	hypothetical prote
23	66.5	17.6	171	2 T29598	hypothetical prote
24	66	17.5	327	2 T00797	hypothetical prote
25	65	17.2	317	2 T70863	hypothetical prote
26	65	17.2	746	2 G02838	enhancer of zeste
27	64.5	17.1	437	2 T28180	hypothetical prote
28	64.5	17.1	903	2 T20804	hypothetical prote
29	64	16.9	417	2 S51961	FUN50 protein ye

ALIGNMENTS

RESULT 1

152718
gene p27kip1 protein - human
C:Species: Homo sapiens (man)
C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
C:Accession: 152718
R:Pietepol, J.A.; Bohlander, S.K.; Sato, Y.; Papadopoulos, N.; Liu, B.; Friedman, C.
Cancer Res. 55, 1206-1210, 1995
A:Title: Assignment of the human p27kip1 gene to 12p13 and its analysis in leukemias.
A:Reference number: 152718; MUID:95188144; PMID:7882309
A:Accession: 152718
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-198 <R>
A:Cross-references: GB:S76988; NID:3998402, PIDN:AA14244.1, PID:94261944
C:Genetics:
A:Gene: p27kip1
A:Introns: 159/1

Query Match 94.4% Score 357; DB 2; Length 198;
Best Local Similarity 94.0% Pred. No. 2.5e-32;
Matches 63; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Q7 1 EYKPSACPNLFQVNHDELTRLEKRRDMEASQRKWNFDQNIKPLEGYEWEVEK 60
DB 22 DHPKPSACPNLFQVNHDELTRLEKRRDMEASQRKWNFDQNIKPLEGYEWEVEK 81
Q7 61 GSLEPEFY 67
DB 82 GSLEPEFY 88

RESULT 2

149064
cyclin, cdk inhibitor p27 - mouse
N:Alternative names: p27, p27, G1 cyclin-cyclin-dependent kinase inhibitor p27
C:Species: Mus musculus (house mouse)
C>Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 05-Nov-1999
C:Accession: 149064
R:Toyoshima, H.; Hunter, T.
Cell 78, 67-74, 1994
A:Title: p27, a novel inhibitor of G1 cyclin-cdk protein kinase activity, is related
A:Reference number: A54839; MUID:9436519; PMID:8033213
A:Accession: 149064
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-197 <R>
A:Cross-references: EMBL:U10446, NID:3532771, PIDN:AAA21144.1, PID:9532772
C:Keywords: cell cycle control
Query Match 94.2% Score 356; DB 2; Length 197;
Best Local Similarity 92.5% Pred. No. 3.4e-32;

Hum. Mol. Genet. 4, 1089-1092, 1995
 A:Title: Two variants of the Cipl/Waf1 gene occur together and are associated with human
 A:Reference number: I54380; MUID:95384154; PMID:7655464
 A:Accession: I68674
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-181 <RES>
 A:Cross-references: GB:147233; MID:9296078; PIDN:AAH59559.1; PID:q986879
 R:Harper, J.W.; Adams, G.R.; Wei, N.; Kiyomarsi, K.; Elledge, S.J.
 Cell 75, 805-816, 1993
 A:Title: The p21 cdk-interacting protein Cipl is a potent inhibitor of G1 cyclin-dependent
 A:Reference number: A49437; MUID:94061996; PMID:8242751
 A:Accession: A49437
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 18-181 <RES>
 A:Cross-references: GB:126165; MID:9455142; PIDN:AAAL6109.1; FID:q455143
 R:Noda, A.; Ning, Y.; Venable, S.F.; Pereira-Smith, O.M.; Smith, J.R.
 Exp. Cell Res. 211, 90-98, 1994
 A:Title: Cloning of sequenced cell-derived inhibitors of DNA synthesis using an expressed
 A:Reference number: I53412; MUID:94170884; PMID:8125163
 A:Accession: I53412
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 18-181 <RES>
 A:Cross-references: GB:126165; MID:9455142; PIDN:AAAL6109.1; FID:q455143
 P:Xiong, Y.; Hancock, G.J.; Zhang, H.; Casse, D.; Kobayashi, F.; Beach, D.
 Nature 366, 701-704, 1993
 A:Title: p21 is a universal inhibitor of cyclin kinases
 A:Reference number: S39357; MUID:94081955; PMID:8259214
 A:Accession: S39357
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 18-181 <RES>
 A:Cross-references: GB:126165; MID:9455142; PIDN:AAAL6109.1; FID:q455143
 C:Genetics:
 A:Gene: Cipl/Waf1

Query Match 39.2%; Score 148; DB 2; Length 181;
 Best Local Similarity 42.6%; Pred. No. 3.8e-09;
 Matches 26, Conservative 11, Mismatches 24, Indels 0, Gaps 0.

QY 7 ACRLLFGPVNHFFLTDLEKHKHMFEEASQPKNFFDQNHKPLEGKYEWGVEKGSILPEF 56
 DB 34 ACRLLFGPVNHFFLTDLEKHKHMFEEASQPKNFFDQNHKPLEGKYEWGVEKGSILPEF 93
 QY 67 Y 67
 DB 94 Y 94

RESULT 8
 I54380
 cyclin-dependent kinase - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 02-Jul-1994 #sequence_revision 02-Jul-1995 #text_change 21-Jul-2000
 C:Accession: I54380
 R:Mousses, S.; Ozcelik, H.; Lee, P.D.; Malkin, D.; Ball, S.B.; Andralis, I.L.
 Hum. Mol. Genet. 4, 1089-1092, 1995
 A:Title: Two variants of the Cipl/Waf1 gene occur together and are associated with human
 A:Reference number: I54380; MUID:95384154; PMID:7655464
 A:Accession: I54380
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-181 <RES>
 A:Cross-references: GB:147233; MID:9296078; PIDN:AAH59559.1; FID:q986879
 C:Genetics:
 A:Gene: Cipl/Waf1

Query Match 38.6%; Score 146; DB 2; Length 181;
 Best Local Similarity 42.6%; Pred. No. 6.4e-09;
 Matches 26, Conservative 10, Mismatches 25, Indels 0, Gaps 0.

QY 7 ACRLLFGPVNHFFLTDLEKHKHMFEEASQPKNFFDQNHKPLEGKYEWGVEKGSILPEF 56
 DB 34 ACRLLFGPVNHFFLTDLEKHKHMFEEASQPKNFFDQNHKPLEGKYEWGVEKGSILPEF 93
 QY 67 Y 67
 DB 94 Y 94

RESULT 9
 I49023
 tumor suppressor p21 Waf1/Cip1 [imported] - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Jun-2000
 C:Accession: I49023; I49296
 R:Huppi, K.; Siwarski, D.; Desik, J.; Michl, P.; Chedid, M.; Reed, S.; Mock, B.; G.
 Oncogene 9, 3017-3020, 1994
 A:Title: Molecular cloning, sequencing, chromosomal localization and expression of mo
 A:Reference number: I49023; MUID:94366761; PMID:8084607
 A:Accession: I49023
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-159 <RES>
 A:Cross-references: EMBL:U09507; MID:q595302; PIDN:AAH60456.1; PID:q595303
 R:El-Deiry, W.S.; Tokino, T.; Waldman, T.; Velculescu, V.; Lin, J.D.; Burrell, M.;
 Cancer Res. 55, 2913-2919, 1995
 A:Title: T4014: clonal control of p21Waf1/Cip1 expression in normal and neoplastic tiss
 A:Reference number: I49296; MUID:95316868; PMID:7796420
 A:Accession: I49296
 A:Status: nucleic acid sequence not shown, translation not shown, translated from GB/
 A:Molecule type: mRNA
 A:Residues: 1-159 <RES>
 A:Cross-references: EMBL:U04174; MID:9902578; PIDN:AA252220.1; FID:9902579
 C:Genetics:
 A:Gene: Waf1

Query Match 37.3%; Score 141; DB 2; Length 159;
 Best Local Similarity 39.1%; Pred. No. 2e-08;
 Matches 25, Conservative 11, Mismatches 28, Indels 0, Gaps 0.

QY 4 KPSAQMILGPGVNHFFLTDLEKHKHMFEEASQPKNFFDQNHKPLEGKYEWGVEKGSIL 63
 DB 13 KPSAQMILGPGVNHFFLTDLEKHKHMFEEASQPKNFFDQNHKPLEGKYEWGVEKGSIL 72
 QY 64 PEYF 67
 DB 73 PKVY 76

RESULT 10
 A49438
 p53 tumor suppressor mediator Waf1 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
 C:Accession: A49438
 R:El-Deiry, W.S.; Tokino, T.; Velculescu, V.E.; Levy, D.R.; Parsons, R.; Trent, J.M.;
 Cell 75, 817-825, 1993
 A:Title: Waf1, a potential mediator of p53 tumor suppression.
 A:Reference number: A49438; MUID:94061997; PMID:8242752
 A:Accession: A49438
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-143 <ELL>
 A:Note: sequence extracted from NCI backbone (NCIN 140007; NCI-P140008)

Query Match 36.5%; Score 138; DB 2; Length 143;
 Best Local Similarity 37.5%; Pred. No. 3.8e-08;
 Matches 24, Conservative 13, Mismatches 27, Indels 0, Gaps 0.

QY 4 KPSAQMILGPGVNHFFLTDLEKHKHMFEEASQPKNFFDQNHKPLEGKYEWGVEKGSIL 63
 DB 13 KPSAQMILGPGVNHFFLTDLEKHKHMFEEASQPKNFFDQNHKPLEGKYEWGVEKGSIL 72

N:Alternate names: hypothetical protein N3555
 C:Species: Saccharomyces cerevisiae
 C>Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 19-Apr-2002
 C:Accession: S63401
 R:Buerscherhoeff, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
 submitted to the Protein Sequence Database, April 1996
 A:Reference number: S62944
 A:Accession: S63401
 A:Molecule type: DNA
 A:Residues: 1-489 <DUE>
 A:Cross-references: EMBL:U77174; RefSeq:U77174; FID:0249869; FID:03502602; JSPDB:GN000014;
 C:Experimental source: strain S288C
 C:Genetics:
 A:Gene: MIPS:YNR069c
 A:Cross-references: SGD:S0005352
 A:Map position: 14R

Query Match 19.4% Score 73.5; DB 2; Length 489;
 Best Local Similarity 25.3%; Pred. NO. 2.3;
 Matches 20; Conservative 10; Mismatches 14; Indels 35; Gaps 3;
 QY 14 PVNHEELIKRLEK-----HRRDMFEASQKKNEDFQNHKP 48
 DB 413 PISREKCLKLEDFDIEIANRLGKIEKYFSKIERAIPHKEDIQENRS-----DQLSP 466
 QY 49 LEGKYEWQV-----EKSL 63
 DB 467 LRGKYEWNAVAGNTENGIL 485

Search completed: May 30, 2003, 09:02:47
 Job time : 6.62662 secs

GenCore version 5.1.6
Copyright (c) 1993-2003 Seq-Map, Inc.

OM protein - protein search, using sw model

Run on: May 30, 2003, 08:52:42, Search time: 2.8555 seconds
(without alignments)
972 808 Million full updates/sec

Title: US-09-865-018b-6_copy_22_88
Perfect score: 378
Sequence: 1 EYKPSACNLEGFVNHEEL.....PLFGKYRWQFVEKSLPEFY 67

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	378	100.0	178	1 CDNB_MUSVI	P46529 mustela vis
2	470	97.9	198	1 CDNB_FELCA	O19001 felis silve
3	360	95.2	198	1 CDNB_HUMAN	P46527 homo sapien
4	356	94.2	197	1 CDNB_MOUSE	P46414 mus musculu
5	351	92.9	198	1 CDNB_CRICR	Q60439 cricetus
6	176	46.6	316	1 CDNC_HUMAN	Q60418 homo sapien
7	168	44.4	348	1 CDNC_MOUSE	P49419 mus musculu
8	148	39.2	164	1 CDNL_HUMAN	P49436 homo sapien
9	144	38.1	164	1 CDNL_FELCA	O19002 felis silve
10	141	37.3	159	1 CDNL_MOUSE	P39689 mus musculu
11	74.5	19.7	532	1 PHP_POTTP	Q28811 pototous tr
12	73.5	19.4	484	1 YN9A_YEAST	P54755 saccharomyc
13	66.5	17.6	171	1 YS01_CAEEL	Q9XV44 caenorhabdi
14	65	17.2	1129	1 UBPC_SCHPO	Q00111 schizosacch
15	64	16.9	417	1 YAC2_YEAST	P49214 saccharomyc
16	63.5	16.8	808	1 SUS1_DAFCA	P44035 daucus caro
17	63	16.7	261	1 YC92_HAEIN	P44154 haemophilus
18	63	16.7	886	1 SXNE_HUMAN	Q9Y5W7 homo sapien
19	63	16.7	899	1 YABD_SCHPO	Q09778 schizosacch
20	62.5	16.5	611	1 IF4B_HUMAN	P23588 homo sapien
21	62	16.4	746	1 E2H2_HUMAN	Q15910 homo sapien
22	61.5	16.3	125	1 FR32_OHWE	Q97323 thiosophila
23	61.5	16.3	956	1 CB31_YEAST	P32504 saccharomyc
24	61	16.1	282	1 PNMT_HUMAN	P11086 homo sapien
25	61	16.1	584	1 ENVI_HUMAN	P10267 homo sapien
26	60.5	16.0	380	1 NTG2_YEAST	Q08214 saccharomyc
27	60.5	16.0	333	1 K2E2_HUMAN	Q96114 homo sapien
28	60	15.9	612	1 DNK1_LISIN	Q92608 listeria in
29	60	15.9	517	1 PNAT_LISIN	Q95541 listeria mo
30	60	15.9	751	1 Z184_HUMAN	Q95676 homo sapien
31	60	15.9	1513	1 PPOD_OPYSA	P12093 opyza sativ
32	59.5	15.7	301	1 OMPG_ECOLI	P76045 escherichia
33	59.5	15.7	358	1 ARCB_CORPS	P96749 corynebacta

ALIGNMENTS

RESULT 1

ID	CDNB_MUSVI	STANDARD;	PRT;	178 AA.
AC	P46529;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase inhibitor p27) (p27Kip1) (Fragment).			
GN	CDKN1B.			
OS	Mustela vison (American mink).			
OC	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;			
OC	Mustela.			
UX	NCB1_faxID=9667;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RX	MEDLINE=94306518; PubMed=8033212;			
RA	Polyak K, Lee M-H, Friedman-Hromage H, Koff A, Roberts J M,			
RA	Tempest P., Massague J.;			
RI	"Cloning of p27Kip1, a cyclin-dependent kinase inhibitor and a			
RT	potential mediator of extracellular antimetogenic signals.";			
RL	Cell 78:59-66(1994).			
RN	[2]			
RP	FUNCTION.			
RX	MEDLINE=94116862; PubMed=8288131;			
RA	Polyak K, Katu T-Y, Solomon M I, Sherr CJ, Massague J.,			
RA	Roberts J.M., Koff A.;			
RT	"p27Kip1, a cyclin-Cdk inhibitor, links transforming growth			
RT	factor-beta and contact inhibition to cell cycle arrest ";			
RL	Genes Dev 8:9-22(1994).			
CC	-1- FUNCTION: Involved in G1 arrest. May mediate TGF beta-induced G1			
CC	arrest. Binds to and inhibits complexes formed by cyclin E/Cdk2,			
CC	Cyclin A/Cdk2, and cyclin D1/Cdk4. Interaction with nucleoporin			
CC	NUP50 is required for nuclear import and for degradation of			
CC	phosphorylated p27Kip1 after nuclear import. (By similarity)			
CC	-1- SUBUNIT: Interacts with Nup50 (by similarity).			
CC	-1- SUBCELLULAR LOCATION: Nuclear			
CC	-1- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.			
CC	-----			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: U00004. AAA0234.1.			
DR	InterPro: IPR003175; CDI.			
DR	Itam; PF02234, CDI, 1.			
KW	Cell cycle; Nuclear protein.			
FT	DOMAIN 153 169 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).			
FT	NON_TER 178 178			
SEQUENCE	178 AA: 40129 MW: 11691C84AD10473E CRC64;			

DR EMBL: AF480891; AAL78041.1; -
DR PDB: 1J5U; 29-JUL-97;
DR SWISS-2DPAGE: P46527; HUMAN.
DR Genbank: U09998; CDK1b
DR MIM: 600778; -
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1.
DR Cell cycle; Nuclear protein; 3D-structure; Polymorphism.
KW DOMAIN 153 169 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
FT VARIANT 15 15 R->W (IN DBSNP:2066827).
FT VARIANT 100 100 V->G (IN DBSNP:2066827).
FT VARIANT 22 22 /FIELD=VAR_Q13A72
FT CONFLICT 153 169 E>D (IN REF. 2).
SQ SEQUENCE 197 AA; 22073 MW; 111805690114F36C QW64;

Query Match 95.2%; Score 360; DB 1; Length 198;
Best Local Similarity 95.5%; Pred. NC: 5.2e-32;
Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKPSACNLFQGVNHEELTRLEKHKRMEEASQKKNFDFQNHKPLEGKYEWQVEK 60
DB 22 EHPKPSACNLFQGVNHEELTRLEKHKRMEEASQKKNFDFQNHKPLEGKYEWQVEK 81

QY 61 GSLPEFY 67
DB 82 GSLPEFY 88

RESULT 4
CDNB_MOUSE STANDARD; PRT; 197 AA.
AC P46414;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cyclin dependent kinase inhibitor 1B (Cyclin-dependent kinase
inhibitor p27) (p27Kip1).
GN CDKN1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9406519; PubMed=833013
RA Toyoshima H., Hunter T.,
RT "p27, a novel inhibitor of G1 cyclin-Cdk protein kinase activity, is
related to p21".
RT Cell 78:67-74(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
RA Polyak K., Lee M.-H., Eridjument-Bromage H., Koff A., Roberts J.M.,
RA Tempest P., Massague J.,
RT "Cloning of p27Kip1, a cyclin-dependent kinase inhibitor and a
potential mediator of extracellular antimitogenic signals".
RT Cell 78:59-66(1994).
RN [3]
RP INTERACTION WITH NUP50, AND MUTAGENESIS.
RX STRAIN=BA1B/C;
RX MEDLINE=20271857; PubMed=10811608.
RA Mueller D., Thiele K., Huerquin A., Diekmann A., Eilers M.;
RT "Cyclin E-mediated elimination of p27 requires its interaction with
the nuclear pore-associated protein MNPAP50".
PL EMBO J. 19:2168-2180(2000).
CC -!- FUNCTION: Involved in G1 arrest. May mediate TGF beta-induced G1
arrest. Binds to and inhibits complexes formed by cyclin E-CDK2,
cyclin A-CDK2, and cyclin E1-CDK4. Interaction with nucleoporin
NUP50 is required for nuclear import and for degradation of
phosphorylated p27Kip1 after nuclear import.
CC -!- SUBUNIT: Interacts with NUP50 (By similarity).
CC -!- SURCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@sib-sib.ch).

CC -!- SURCELLULAR LOCATION: Nuclear
CC -!- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@sib-sib.ch).

CC EMBL: U10440; AAA21149.1; -
CC EMBL: U09998; AAA2235.1; -
CC MIM: 60104565; Cdkn1b
CC InterPro: IPR003175; CDI.
CC Pfam: PF02234; CDI; 1.
CC Cell cycle; Nuclear protein.
KW DOMAIN 153 169 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
FT MUTAGEN 90 90 R->S; LOSS OF INTERACTION WITH NUP50.
SQ SEQUENCE 197 AA; 22110 MW; 2D19A6CFE6EA650D CRC64;

Query Match 94.2%; Score 356; DB 1; Length 197;
Best Local Similarity 92.5%; Pred. NC: 5.2e-32;
Matches 62; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKPSACNLFQGVNHEELTRLEKHKRMEEASQKKNFDFQNHKPLEGKYEWQVEK 60
DB 22 EHPKPSACNLFQGVNHEELTRLEKHKRMEEASQKKNFDFQNHKPLEGKYEWQVEK 81

QY 61 GSLPEFY 67
DB 82 GSLPEFY 88

RESULT 5
CDNB_CRIGR STANDARD; PRT; 198 AA
ID "UNP_CPI1P
AC Q60439;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cyclin dependent kinase inhibitor 1B (Cyclin-dependent kinase
inhibitor p27) (p27Kip1) (P30 KIP1).
GN CDKN1B OR KIP1.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung;
RX MEDLINE=97471701; PubMed=9330642;
RA Parekh H.P., Pillarisetti K., Kunapuli S., Simpkins H.;
RT "Isolation of a hamster cDNA homologous to the mouse and human cyclin
kinase inhibitory protein p27Kip1".
RA Somat Cell Molec Genet. 23:147-151(1997)
CC -!- FUNCTION: Involved in G1 arrest. May mediate TGF beta-induced G1
arrest. Binds to and inhibits complexes formed by cyclin E-CDK2,
cyclin A-CDK2, and cyclin E1-CDK4. Interaction with nucleoporin
NUP50 is required for nuclear import and for degradation of
phosphorylated p27Kip1 after nuclear import (By similarity).
CC -!- SUBUNIT: Interacts with NUP50 (By similarity).
CC -!- SURCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@sib-sib.ch).


```

RX MEDLINE=95247028; PubMed=7729664;
RA Matsuo S., Edwards M.C., Bai C., Parker S., Zhang P., Baldini A ,
RA Harper J.W., Elledge S.J.;
RT "p57KIP2, a structurally distinct member of the p21CIP1 Cdk inhibitor
RT family, is a candidate tumor suppressor gene.";
RL Genes Dev. 9:650-662(1995).
CC
CC -1- FUNCTION: POTENT TIGHT-BINDING INHIBITOR OF SEVERAL G1 CYCLIN/CDK
CC COMPLEXES (CYCLIN E-CDK2, CYCLIN D2-CDK4, AND CYCLIN A-CDK2) AND,
CC TO LESSER EXTENT, OF THE MITOTIC CYCLIN B-CDK2. NEGATIVE REGULATOR
CC OF CELL PROLIFERATION. MAY PLAY A ROLE IN MAINTENANCE OF THE
CC NONPROLIFERATIVE STATE THROUGHOUT LIFE.
CC
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC
CC -1- TISSUE SPECIFICITY: IT IS EXPRESSED IN THE HEART, BRAIN, LUNG,
CC SKELETAL MUSCLE, KIDNEY, PANCREAS AND TESTIS. HIGH LEVELS ARE SEEN
CC IN THE PLACENTA WHILE LOW LEVELS ARE SEEN IN THE LIVER.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL: U20553; AAC52186.1; -
CC EMBL: U22399; AA85096.1; -
CC MGD: MGI:104564; Cdkkl.
CC InterPro, IPRO03175; Cdk.
CC Pfam: PF02234; Cdk1; 1.
CC
CC Cell cycle; Alternative splicing
CC
CC DOMAIN 108 189 PRO-RICH.
CC DOMAIN 178 284 GLU/ASP RICH.
CC
CC FT DOMAIN 309 312 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
CC FT VARSPPLIC 1 13 MISSING (IN ISOFORM KIP2H/P57B).
CC FT CONFLICT 150 151 DA -> EP (IN REF. 2).
CC
CC SQ SEQUENCE 348 AA: 37331 MW: 10845381/7701604 ckw64;
CC
CC Query Match 44.4%; Score 168; DB 1; Length 348;
CC Best Local Similarity 45.5%; Pred. No. 3.4e-11;
CC Matches 30; Conservative 13; Mismatches 21; Indels 2; Gaps 1;
CC
CC QY 4 KPSACENLPGVNHRELTHLEKHPDMEFASQPKWNEFQNHKPLE--GRYWECEVERK 61
CC DB 28 KSAACFSPSPVWREELAFELDPMPLEIAELNAELINWLENFQVGLVPLPSPPLWMEVUSE 87
CC
CC QY 62 SLPEFY 67
CC I: I I I
CC DB 88 SVPAFY 93
CC
CC RESULT 8
CC CUNI_HUMAN STANDARD; PRT; 164 AA.
CC AC P38936; Q9B0T4;
CC DT 01-FEB-1995 (Rel. 31, Created)
CC DT 01-FEB-1995 (Rel. 31, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Cyclin dependent kinase inhibitor 1 (p21) (CDK interacting protein 1)
CC DE (Melanoma differentiation associated protein 6) (MDA-6).
CC GN CDKNIA or CDKN1 or CIP1 or WAF1 or MDA6 or SDI1 or P21 or CAP20.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC
CC NCBI_TaxID=9606;
CC
CC [1]
CC SEQUENCE FROM N.A.
CC RX MEDLINE=94061996; PubMed=8242751;
CC RA Harper J.W., Adami G.F., Wei N., Koyama S.J.;
CC RT "The p21 Cdk interacting protein Cipl1 is a potent inhibitor of G1
CC cyclin-dependent kinases.";
CC RL Cell 75:805-816(1993)
CC
CC SEQUENCE FROM N.A.

```

```

FX MEDLINE=94061997; PubMed=8242752;
RA El-Deiry W.S., Tokino T., Velculescu V.E., Levy D.B., Parsons P.,
RA Trent J.M., Lin D., Mercer W.E., Kinzler K.W., Vogelstein B.;
RT "WAF1, a potential mediator of p53 tumor suppression.";
RL Cell 75:817-825(1993).
CC
CC [3]
CC SEQUENCE FROM N.A.
CC RX MEDLINE=94081955; PubMed=8254214;
CC Xiong Y., Hannon G.J., Zhang H., Casso D., Kobayashi R., Beach D.;
CC RT "p21 is a universal inhibitor of cyclin kinases.";
CC RL Nature 366:701-704(1993).
CC
CC [4]
CC SEQUENCE FROM N.A.
CC RA Jiang H., Fisher P.B.;
CC RT "Use of a sensitive and efficient subtraction hybridization protocol
CC for the identification of genes differentially regulated during the
CC induction of differentiation in human melanoma cells.";
CC RL Mol. Cell. Differ. 1:285-294(1994).
CC
CC [5]
CC SEQUENCE FROM N.A.
CC RA Jiang H., Lin T., Herlyn M., Kerbel P.S., Weissman B.E.,
CC Welch D.P., Fisher P.B.;
CC RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
CC
CC [6]
CC SEQUENCE FROM N.A.
CC RX MEDLINE=9417884; PubMed=8125163;
CC Noda A., Ning Y., Venable S.F., Pereira-Smith O.M., Smith J.R.;
CC RT "Cloning of senescent cell-derived inhibitors of DNA synthesis using
CC an expression screenet.";
CC RL Exp. Cell Res. 211:90-98(1994).
CC
CC [7]
CC SEQUENCE FROM N.A.
CC RX MEDLINE=95384154; PubMed=7655464;
CC Mousses S., Oezcelik H., Lee P.D., Malkin D., Poll S.P.,
CC Andrulis I.L.;
CC RT "Two variants of the CIP1/WAF1 gene occur together and are associated
CC with human cancer.";
CC RL Hum. Mol. Genet. 4:1089-1092(1995).
CC
CC [8]
CC SEQUENCE FROM N.A., AND VARIANT ARG-31.
CC RA Rieder M.J., Braun A.C., Montoya M.A., Chung M.-W., Nguyen C.P.,
CC Nguyen D.A., Livingston P.T., Pool C.L., Robertson P.D.,
CC Schachlitz W.S., Sherwood J.K., Wittrik L.A., Nickerson N.A.;
CC RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC
CC [9]
CC SEQUENCE FROM N.A.
CC RA Palmer S.;
CC RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC
CC [10]
CC SEQUENCE FROM N.A., AND VARIANT ARG-31
CC RA Straussberg R.;
CC RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC
CC [11]
CC X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 139-160
CC MFOLINE=97015085; PubMed=8661913;
CC Curtis J.M., Kelman Z., Horwitz I., O'Donnell M., Kiriyan I.;
CC RT "Structure of the C-terminal region of p21(WAF1/CIP1) complexed with
CC human PCNA.";
CC RL Cell 87:297-306(1996).
CC
CC -1- FUNCTION: MAY BE THE IMPORTANT INTERMEDIATE BY WHICH P53 MEDIATES
CC ITS ROLE AS AN INHIBITOR OF CELLULAR PROLIFERATION IN RESPONSE TO
CC DNA DAMAGE. MAY BIND TO AND INHIBIT CYCLIN-DEPENDENT KINASE
CC ACTIVITY, PREVENTING PHOSPHORYLATION OF CRITICAL CYCLIN-DEPENDENT
CC KINASE SUBSTRATES AND BLOCKING CELL CYCLE PROGRESSION.
CC
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC
CC -1- TISSUE SPECIFICITY: IS EXPRESSED IN ALL ADULT HUMAN TISSUES,
CC WITH 5-FOLD LOWER LEVELS OBSERVED IN THE BRAIN.
CC
CC -1- INDUCTION: BY P53, MYOERIN (ANTITUMORIC COMPOUND) AND INTERFERON
CC BETA.
CC
CC -1- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.
CC
CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/CDKN1AID139.html".

```


Cell 75:817 825(1993).

CC -1- FUNCTION: MAY BE THE IMPORTANT INTERMEDIATE BY WHICH P53 MEDIATES ITS ROLE AS AN INHIBITOR OF CELLULAR PROLIFERATION IN RESPONSE TO DNA DAMAGE. MAY BIND TO AND INHIBIT CYCLIN-DEPENDENT KINASE ACTIVITY, PREVENTING PHOSPHORYLATION OF CRITICAL CYCLIN-DEPENDENT KINASE SUBSTRATES AND BLOCKING CELL CYCLE PROGRESSION.

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- INDUCTION: BY P53, MEZEREIN (ANTI-NEKEMIC COMPOUNT) AND INTERFERON BETA.

CC -1- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL: U09507; AAC6456.1; 1.
EMBL: U24173; AAC52230.1; 1.
DR PIR: A49438; A49438.
DR MG: MG1:104556; GdKala.
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1.
KW Cell cycle; Nuclear protein; Zinc-finger.
FT ZN-FING 12 43 C4-TYPE (POTENTIAL).
FT CONFLICT 30 30 F -> S (IN REF. 3).
FT CONFLICT 56 57 TP -> RQ (IN REF. 3).
SU SEQUENCE 159 AA; 17785 MW; 3787C22B9A2F5089 CRC64.

Query Match 37.3%; Score 141; DB 1; Length 159;
Best Local Similarity 39.1%; Pred. No. 1.3e-08;
Matches 25; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

QY 4 KPSACHNLEPGVNHLELTPDLEKHPFWEASQPKWNFQNHKPLECKYEWQVEKCSL 63
DB 13 RSKVCEIFGPVESELELPGHCHALMAGELYEAFERWNFDFVTEPLEGFWVERKSL 72

QY 64 PEY 67
DB 73 PKVY 76

RESULT 11

PHR_POTTR STANDARD: PRT: 532 AA.

AC Q28811;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Deoxyribodipyrimidine photolyase (6' 4' 1' 9' 3') (DNA photolyase)
DE (Photoreactivating enzyme).
OS Porosus tridactylus (Potoso).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Metatheria; Diprotodontia; Macroplodidae; Peromysci
CC NCBI_TaxID=9310;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95112925; PubMed=7813451;
FA Yagci A., Eker A.F., Yasutaka S., Yajima H., Kobayashi T., Takao M.,
RA Okawa A.;
RT "A new class of DNA photolyases present in various organisms including apical mammals."

RL EMBL J. 13:6143-6151(1994).

CC -1- FUNCTION: THIS ENZYME CATALYZES THE LIGHT-DEPENDENT MONOMERIZATION (300-600 NM) OF CYCLOHUIYL PYRIMIDINE DIMERS (IN CIS-SYN CONFIGURATION), WHICH ARE FORMED BETWEEN ADJACENT BASES ON THE SAME DNA STRAND, UPON EXPOSURE TO ULTRAVIOLET RADIATION.

CC -1- CATALYTIC ACTIVITY: Cyclobutadipyrimidine (in DNA) + 2 pyrimidine residues (in DNA).

CC -1- COFACTOR: FAD.

CC -1- SIMILARITY: BELONGS TO THE DNA PHOTOLYASE CLASS-2 FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL: P26020; PAA05041.1; 1.
DR InterPro: IPR000474; DNA_photolyase.
DR InterPro: IPR000288; DNA_photolyase_2.
DR InterPro: IPR005101; FAD binding_7.
DR Pfam: PF00875; DNA_photolyase; 1.
DR Pfam: PF03441; FAD binding_7; 1.
DR ProDom: PD007711; DNA_photolyase_2; 1.
DR TIGRFAMs: TIGR00591; phr2; 1.
DR PROSITE: PS01083; DNA_PHOTOLYASES_2; 1.
DR PROSITE: PS01084; DNA_PHOTOLYASES_2; 1.
KW Lyase, Chromophore, Flavoprotein; FAD, DNA repair, DNA-binding.
SU SEQUENCE 542 AA; 6163 MW; 0805B1BFE7B625B CRC64.

Query Match 19.7%; Score 74.5; DB 1; Length 532;
Best Local Similarity 29.5%; Pred. No. 0.9;
Matches 26; Conservative 11; Mismatches 28; Indels 23; Gaps 5;

QY 3 PKPSACHNLEPGVNHLELTPDLEKHPFWEASQPKWNFQNHKPLECKYEWQVEKCSL 63
DB 325 PNKIALSNLSFWFHEGQVSVQPAITLVQKHPSYPDSVTNFVEAVVPPPLAIDNFCYNK 384

QY 45 NKKPLECKYEWQVEV-----EKGSLPEFY 67
DB 385 NYDKLEGAYDWAQTTTLRHAKDKRPHLY 412

RESULT 12

YN98_YEAST STANDARD: PRT: 489 AA.

AC P53755;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 54.8 kDa protein in BIO3-HXT17 intergenic region.
GN YNR069C OR N3555.
OS Saccharomyces cerevisiae (Baker's yeast).
CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
CC NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Duesterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D.,
RA Hilbert H., Moesli D.,
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO THE N-TERMINAL OF YEAST BUL1 AND YML111W.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL: Z71684; CAA96351.1; 1.
DR SGD: S0005352; YNR069C.
KW Hypothetical protein.
SU SEQUENCE 489 AA; 54831 MW; F065789F1C4F874 CRC64.

Query Match 19.4%; Score 73.5; DB 1; Length 489;
Best Local Similarity 25.3%; Pred. No. 1.1;
Matches 20; Conservative 10; Mismatches 14; Indels 35; Gaps 3;

QY 14 PVNHEULTRDLEK-----HRPDMEEASQKWNDFQNHK 48


```
RESULT 15
YAG1_YEAST
ID YAG1_YEAST STANDARD; PRT; 417 AA.
AC P39713;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Hypothetical zinc-type alcohol dehydrogenase-like protein in GDH3-CNE1
DE intergenic region.
GN YAL061W OR FUN50.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID:4932;
RN [1]
SEQUENCE FROM N.A.
PC STRAIN-S288C / AB972;
KC MEDLINE:95249563; PubMed:7731988;
RA Hussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
RA Hall J., Guelliette B.F.F., Keng T., Barton A.B., Su Y., Davies C.K.,
RA Storms K.K.;
RT "The nucleotide sequence of chromosome I from Saccharomyces
RT cerevisiae."
RL Proc. Natl. Acad. Sci. U S A 92:3809-3813(1995).
CC -|- COPACITOR: ZINC (Potential).
CC -|- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U12980; AAC04973.1; -.
DR SGD: S0000057; YAL061W.
DR InterPro: IPR002328; ADH_zinc.
DR InterPro: IPR002085; Adh_zn_family.
DR Pfam: PF00107; adh_zinc; 1.
DR PROSITE: PS00059; ADH_ZINC; 1.
KW Hypothetical protein; Oxidoreductase; Zinc.
FT METAL 39 39 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 64 64 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 120 120 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 123 123 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 131 131 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 173 173 ZINC (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 417 AA; 46098 MW; D921FD9FA1D0151 CPC64;
Query Match 16.9%; Score 64; DB 1; Length 417;
Best local similarity 14.3%; Pred No 9.6;
Matches 12; Conservative 8; Mismatches 15; Indels 0; Gaps 0;
```

```
QY 4 KPSACRNLFQPVNHEELTRDLKRRHRRMEASQKK 38
| | : | | | | : : : | |
Db 366 KESTIKITLTPNNHCELNFEADNEKKFISLSPEK 400
```

Search completed: May 30, 2003, 08:59:13
Job time : 3.85659 secs

GenCode version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd

OM protein - protein search, using sw model

Run on: May 30, 2003, 08:53:57 : Search time 11.686 Seconds
(without alignments)
1181.337 Million cell updates/sec

Title: US-09-865-018b-6_copy_22_88

Perfect score: 478

Sequence: 1 EYKPSACNLFPGVNHLEL.....PLEGKYEWQVEVKGSLPEFY 67

Scoring table: RIGS0M62

Gapop 10 0 0 Gapext 0 5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters. 671580

Minimum DB seq length: 0

Maximum DB seq length: 206000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_protist.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacterioph.*
- 17: sp_archaeap.*

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	370	97.9	172	6	Q9BEA5 Sus scrofa
2	370	97.9	198	6	Q9BDC3 Sus scrofa
3	360	95.2	158	4	Q43806 Homo sapien
4	360	95.2	198	4	Q9NYG6 Homo sapien
5	360	95.2	198	4	Q9RNS6 Homo sapien
6	359	95.0	197	11	Q08769 Rattus norv
7	359	95.0	197	11	Q35792 Rattus norv
8	357	94.4	184	4	Q9B100 Homo sapien
9	218.5	57.8	179	13	Q9QYX4 Q90x4 brachydact
10	172	45.5	210	13	Q91603 Xenopus lae
11	169	44.7	209	13	Q91646 Xenopus lae
12	168	44.4	335	11	Q91V06 Mus musculu
13	155	41.0	164	11	Q64315 Rattus norv
14	148	39.2	164	4	Q961F1 Homo sapien
15	146	38.6	181	4	Q14010 Homo sapien
16	115.5	30.6	258	5	Q22198 Caenorhabdi

17	108	28.6	259	5	Q9U6R5
18	100	26.5	131	10	Q04154 Arabidopsis
19	100	26.5	191	10	Q82809 Arabidopsis
20	91.5	24.2	253	5	Q8WQ02 Arabidopsis
21	87.5	23.1	184	5	Q22197 Arabidopsis
22	86	22.8	245	5	Q94536 Arabidopsis
23	86	22.8	255	5	Q91654 Arabidopsis
24	85	22.5	163	10	Q93V92 Arabidopsis
25	84	22.2	245	5	Q91668 Arabidopsis
26	81.5	21.6	196	10	Q9JL15 Arabidopsis
27	81	21.4	192	10	Q9FS28 Arabidopsis
28	81	21.4	222	10	Q9FKB5 Arabidopsis
29	77	20.4	156	10	Q93YF6 Arabidopsis
30	77	20.4	189	10	Q9LYK0 Arabidopsis
31	76	20.1	286	10	Q94CM0 Arabidopsis
32	76	20.1	284	10	Q48446 Arabidopsis
33	74.5	19.7	470	6	Q28464 Monodelphis
34	72	19.0	106	6	Q97870 Canis fami
35	72	19.0	647	5	Q9V060 Arabidopsis
36	71.5	18.9	195	10	Q9FX90 Arabidopsis
37	71.5	18.9	195	10	Q94CL9 Arabidopsis
38	71.5	18.9	196	10	Q48597 Arabidopsis
39	69.5	18.4	204	15	Q9YU29 Human immun
40	69	18.4	141	11	Q94P82 Arabidopsis
41	69	18.3	279	5	Q23168 Arabidopsis
42	68	18.0	330	10	Q9SCD8 Arabidopsis
43	67.5	17.9	209	10	Q9SCR2 Arabidopsis
44	67.5	17.9	246	3	Q03973 Saccharomyc
45	67.5	17.9	817	4	Q9H0G4 Homo sapien

ALIGNMENTS

RESULT 1

Q9BEA5 PRELIMINARY; PRT; 172 AA.

AC Q9BEA5; DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE P27K1pl degradation-resistant isoform (Fragment).
GN P27K1PLR.

OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina, Suidae, Sus.
OX NCBI_TaxID=9823;
RN [1]

RP SEQUENCE FROM N.A.

EX MEDLINE=21083196; PubMed=11115598;

FA Hirano K., Hirano M., Zeng Y., Nishimura J., Hara K., Muta K.,

RA Nawata H., Kanaide H.;

RT "Cloning and functional expression of a degradation-resistant novel

RI isoform of p27Kipl.,"

RL Biochem J 353:51-57(2001).

DR EMEL; AR031958; BAB39728.1; -.

DR InterPro: IPR002047; AKH.

DR Pfam: PF02234; CDI; 1.

DR ProSITE: PS00256; AKH; UNKNOWN_1.

FT NON_TER

SQ SEQUENCE 172 AA: 10348 MW: 9882240804446E CPC64;

Query Match: 97.9%, Score 370, Lb 6, Length 172.
Best local similarity: 98.5%, Pred. No. 17e-33,
Matches 66; Conservative 0, Mismatches 1; Indels 0, Gaps 0.

Qy 1 EYKPSACNLFPGVNHLELPLEGKYEWQVEVKGSLPEFY 60

Db 14 EYKPSACNLFPGVNHLELPLEGKYEWQVEVKGSLPEFY 73

Qy 61 GSLPEFY 67

|||||


```

Query Match: 95.2%; Score 360; DB 4; Length 198;
Best Local Similarity 95.5%; Pred. No. 2.6e-32;
Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKPSACRNLPQGVNHELTGKHKHPRMFEASQKKNFDFQNHKPLEGKYEWQVEVK 60
DB 22 EHKPSACRNLPQGVNHELTGKHKHPRMFEASQKKNFDFQNHKPLEGKYEWQVEVK 81

QY 61 GSLPEFY 67
DB 82 GSLPEFY 88

RESULT 6
008769 PRELIMINARY; PRT; 197 AA.
AC 008769;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE P27 K1P1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RA Kawada M., Yamagoe S., Uehara Y.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kawada M., Yamagoe S., Kazuo S., Mizuno S., Uehara Y.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Kawada M., Yamagoe S., Murakami Y., Suzuki K., Mizuno S., Uehara Y.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Dastvan F., Peidy M.A.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: D86924; BAA19460.1; -.
DR EMBL: AF015194; AAB71368.1; -.
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1.
SQ SEQUENCE 197 AA; 22139 MW; 55738078C2D555B2 CRC64;

Query Match: 95.0%; Score 359; DB 11; Length 197;
Best Local Similarity 94.0%; Pred. No. 3.3e-32;
Matches 63; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKPSACRNLPQGVNHELTGKHKHPRMFEASQKKNFDFQNHKPLEGKYEWQVEVK 60
DB 22 EHKPSACRNLPQGVNHELTGKHKHPRMFEASQKKNFDFQNHKPLEGKYEWQVEVK 81

QY 61 GSLPEFY 67
DB 82 GSLPEFY 88

RESULT 7
015792 PRELIMINARY; PRT; 197 AA.
AC 015792;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE P27.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

```

```

RN [1]
RP SEQUENCE FROM N.A.
PC STRAIN=SPRAGUE-DAWLEY; TISSUE=SPLEEN;
PX MFTLINE=97361751; PubMed=9218722;
PA Nomura H., Sawada Y., Fujinaga K., Ohtaki S.;
PT "Cloning and characterization of rat p27kip1, a cyclin-dependent
PI kinase inhibitor."
PL Gene 191:211-218(1997).
DR EMBL: D83792; BAA21561.1; -.
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1.
SQ SEQUENCE 197 AA; 22112 MW; 55738078C2D555B2 CRC64;

Query Match: 95.0%; Score 359; DB 11; Length 197;
Best Local Similarity 94.0%; Pred. No. 3.3e-32;
Matches 63; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKPSACRNLPQGVNHELTGKHKHPRMFEASQKKNFDFQNHKPLEGKYEWQVEVK 60
DB 22 EHKPSACRNLPQGVNHELTGKHKHPRMFEASQKKNFDFQNHKPLEGKYEWQVEVK 81

QY 61 GSLPEFY 67
DB 82 GSLPEFY 88

RESULT 8
096TE0 PRELIMINARY; PRT; 198 AA
AC 096TE0;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Cdk inhibitor p27kip1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MDLINE=2937222; PubMed=10913178;
RA Millard S.S., Vidal A., Markus M., Koff A.;
RT "A Urlich element in the 5' untranslated region is necessary for the
RI translation of p27 mRNA."
RL Mol. Cell. Biol. 20:5947-5959(2000).
DR EMBL: AY04255; AAF88142.1; -.
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1.
SQ SEQUENCE 198 AA; 22017 MW; K1FEF33KAAH248 CPC64;

Query Match: 94.4%; Score 357; DB 4; Length 198;
Best Local Similarity 94.0%; Pred. No. 5.5e-32;
Matches 63; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYKPSACRNLPQGVNHELTGKHKHPRMFEASQKKNFDFQNHKPLEGKYEWQVEVK 60
DB 22 EHKPSACRNLPQGVNHELTGKHKHPRMFEASQKKNFDFQNHKPLEGKYEWQVEVK 81

QY 61 GSLPEFY 67
DB 82 GSLPEFY 88

RESULT 9
090YX4 PRELIMINARY; PRT; 179 AA.
AC 090YX4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE p27-like cyclin-dependent kinase inhibitor.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```



```

[4]
RN  SEQUENCE FROM N.A.
RP  SPECIES=Mouse, TISSUE=BREAST TUMOR;
RC  Scrausberg K.;
RA  Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RL  EMRL: A176505; CAC16402.1; -.
DR  EMBL: AF160190; AAF00683.1; -.
DF  EMBL: BC005412; AAE05412.1; -.
DP  MGD: MGI-104564; Cdkn1c.
DR  InterPro: IPR003175; CDI.
DR  Pfam: PF02234; CDI, 1.
KW  Kinase.
SQ  SEQUENCE 335 AA; 35903 MW; E5C40675287FEB3F CRC64;

Query Match 44.4%; Score 168; DB 11; Length 335;
Best Local Similarity 45.5%; Pred. No. 1.2e-09;
Matches 30; Conservative 13; Mismatches 21; Indels 2; Gaps 1;

QY 4 KPSACNLFGPVNHEELTRDLEKHKRRDMEASQKWNFDQNHKPLEGKYEWQVEKGS 61
DQ : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 15 RSSACRSIFGVPVHFFISPELMPRTAFINAFINQNDNFNFQDQVPLRGKQLQWMEVDSE 74

QY 62 SLPEFY 67
DQ : || || ||
Db 75 SVPAFY 80

RESULT 13
Q64315 PRELIMINARY: PPT; 164 AA.
AC Q64315;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P21 (WAF1).
GN WAF1 OR CIP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
FP MEDLINE=9531644; PubMed=7746420;
RA el-Deiry W.S., Tokino T., Waldman T., Velculescu V., Linner J.D.,
RA Burrell M., Hill D.F., Pees J.L., Hamilton S.P., Kinzler K.W.,
RA Vogelstein B.;
PT "Topological control of p21WAF1/CIP1 expression in normal and
PT neoplastic tissues."
RL Cancer Res. 55:2910-2919(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=F344/N; TISSUE=LUNG;
RA Belinsky S.A.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U24174; AAC52231.1; -.
DR EMBL: U41275; AAC42084.1; -.
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI, 1.
SQ SEQUENCE 164 AA; 18318 MW; 60A7F66045B6435F CRC64;

Query Match 41.0%; Score 155; DB 11; Length 164;
Best Local Similarity 40.6%; Pred. No. 1.2e-09;
Matches 26; Conservative 11; Mismatches 27; Indels 0; Gaps 0;

QY 4 KPSACNLFGPVNHEELTRDLEKHKRRDMEASQKWNFDQNHKPLEGKYEWQVEKGS 63
DQ : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 13 RSKVGRPLFGPVDSQSLRDCDALMASVIGFAPEARNFDFATETPLEGNYWVERSPGL 72

QY 64 PEFY 67
DQ : ||
Db 73 PKLY 76

```

```

RESULT 14
Q96LE1 PRELIMINARY: PRT; 164 AA.
AC Q96LE1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cyclin dependent kinase inhibitor isoform.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li L.-C., Zhao H., Yahya R.;
RT "Cloning and Characterization of p21 Isoform."
RL Submitted (SEF-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY008263; AAG15411.1; -.
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI, 1.
KW Kinase.
SQ SEQUENCE 164 AA; 17827 MW; 378E002161FB3BD7 CRC64;

Query Match 39.2%; Score 148; DB 4; Length 164;
Best Local Similarity 42.6%; Pred. No. 7.5e-09;
Matches 26; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

QY 7 ACRLFGPVNHEELTRDLEKHKRRDMEASQKWNFDQNHKPLEGKYEWQVEKGS 66
DQ : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 17 ACRLFGPVDSQSLRDCDALMAGCIQEARWNFDFVETPLEGDFAWERVRLGLPKL 76

QY 67 Y 67
DQ : ||
Db 77 Y 77

RESULT 15
Q14010 PRELIMINARY: PRT; 181 AA.
AC Q14010;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cyclin-dependent kinase (Fragment).
GN CIP1/WAF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TUMOR;
RX MEDLINE=95384154; PubMed=7655464;
RA Mousses S., Ozcelik H., Lee P.D., Malkin D., Bull S.B., Andrulis J.L.;
RT "Two variants of the CIP1/WAF1 gene occur together and are associated
RT with human cancer."
RL Hum. Mol. Genet. 4:1089-1092(1995).
DR EMBL: L47232; AAB59559.1; -.
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI, 1.
KW Kinase.
FT NON_TER
SV SEQUENCE 181 AA; 20083 MW; 4CCFA5112232D4F1 CRC64;

Query Match 38.6%; Score 146; DB 4; Length 181;
Best Local Similarity 42.6%; Pred. No. 1.4e-08;
Matches 26; Conservative 10; Mismatches 25; Indels 0; Gaps 0;

QY 7 ACRLFGPVNHEELTRDLEKHKRRDMEASQKWNFDQNHKPLEGKYEWQVEKGS 66
DQ : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 34 ACRLFGPVDSQSLRDCDALMAGCIQEARWNFDFVETPLEGDFAWERVRLGLPKL 93

QY 67 Y 67

```

10 64 Y '04

Search completed: May 30, 2004, 09:01:54
Job time : 12.686 Secs